

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 28, 08:38:45 ; Search time 12.9816 Seconds  
(without alignments)  
1051.193 Million cell updates/sec

Title: us-09-730-465-2

Score: 1.0  
Sequence: 1 MWASDGMALGVLSVCL.....VLYNGLKCDKREPTNSN 250

Scoring table: BLOSUM63  
Gap=10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50

Minimum Match 100%

Listing first 45 summaries

Database : 1: PIR+  
2: PIR2+  
3: PIR3+  
4: PIR4+

Pred. No. is the number of results predicted by chance to have a  
score at least as high as the one observed. The results are printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1326	100.0	2	A28564
2	1315	9.5	240	2 J01433
3	1295	24.0	2	A53344
4	123	9.3	243	A53344
5	115.5	8.7	351	1 RHRC22
6	115.5	8.7	351	1 RHRC22
7	105.5	8.0	773	1 ORB66
8	103	7.8	240	2 S01299
9	103	7.8	240	2 S01299
10	103	7.8	240	2 S01299
11	97.5	7.4	1276	2 A21553
12	97.5	7.4	1276	2 A21553
13	97.5	7.4	1276	2 A21553
14	97.5	7.4	1276	2 A21553
15	97.5	7.4	1276	2 A21553
16	97.5	7.4	1276	2 A21553
17	97.5	7.4	1276	2 A21553
18	97.5	7.4	1276	2 A21553
19	97.5	7.4	1276	2 A21553
20	97.5	7.4	1276	2 A21553
21	97.5	7.4	1276	2 A21553
22	97.5	7.4	1276	2 A21553
23	97.5	7.4	1276	2 A21553
24	97.5	7.4	1276	2 A21553
25	97.5	7.4	1276	2 A21553
26	97.5	7.4	1276	2 A21553
27	97.5	7.4	1276	2 A21553
28	97.5	7.4	1276	2 A21553
29	97.5	7.4	1276	2 A21553

protein F52C12.1 [ gene 284 protein - hypothetical protein - neural adhesion pr - hypothetical prote - hypothetical prote - ribonucleoside-dip - kinase-associated - D5 protein - vaccl - P58 protein - vari - ATP-binding pr - hypothetical prote - probable 90.4K pro

## ALIGNMENTS

## RESULT 1

N:lymphocyte function-associated antigen 3, transmembrane splice form precursor - human  
C:Species: Homo sapiens (man)  
C:Accession: A28564, S01269  
B:Walsh, B.P.; Frey, A.Z.; Tizard, R.; Metallano, R.J.; Hession, C.; Sanders, M.E.  
A>Title: Primary structure of lymphocyte function-associated antigen 3 (LFA-3). The 1  
A:Reference number: A28564; MIM:8809714; PMID:3305127  
A:Accession: A28564, S01269  
A:Residues: 1-250 <MAL>  
A:Cross references: DB:00736; MID:g3436; PID:CM46668.1; PID:g3437  
A:Note: The authors translated the codon TAT for residue 34 as Val  
B:Seed, B.  
A:Reference number: S01269; MID:8803074; PMID:331302  
A>Title: An LFA-3 cDNA encodes a phospholipid-linked membrane protein homologous to 1  
A:Residues: 1-235, 'VL' <SEE>  
A:Accession: S01269  
C:Cross references: EMBL:X0296; MID:g3439; PID:CM46622.1; PID:g3430  
C:Comment: For an alternative splice form, see PIR:A28564.  
G:Genetic: cDNA, EP3  
A:Cross references: DB:120380; OMIM:153420  
A:Map position: lpl-1p13  
A:Superfamily: human v-cell antigen CD19; immunoglobulin heavy  
F:1-35/Product: signal sequence status predicted <SIC>  
F:31-25/Product: lymphocyte function-associated antigen 3 transmembrane splice form  
F:40.94.109.135.135/Binding site: carbohydrate (Amm) (covalent) status predicted  
Query Match 100.0% Size: 236, DB 2, Length 250.  
Best Local Similarity 100.0% Prod No. 2, ac-105  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MWASDGMALGVLSVCLRGTFISQGIQYGVYGVNVPSPVLEWAKKK 60  
DB 61 DWALENSFRFSPKRNVLVDSUTYATNSDEBETDNESPTDNKTFELV 120  
DB 61 DWALENSFRFSPKRNVLVDSUTYATNSDEBETDNESPTDNKTFELV 120  
OY 121 LESLSPFLTCALNTNSVQCMIPETVNSHGLNWSMCMQCMKNSSTVFMEND 180











A>Title: Amino acid sequence of two functional sites in yeast glycogen phosphorylase.  
 A:Reference number: S32596; MID:75146541; PMID:1092346  
 A:Molecule type: protein  
 A:Residues: 1-18; R'-20-24; 30-37; 77-754 <LRS>  
 A:Check: 13-18; R'-20-24; 30-37; 77-754; E.  
 Arch: Biochem. Biophys. 221:669-678, 1993  
 A>Title: Purification and properties of phosphorylase from baker's yeast.  
 A:Reference number: S32597; MID:84622569; PMID:8354094  
 A:Molecule type: protein  
 A:Residues: 'X', 38-39, 'X', 41-48 <RCS>  
 A:Check: 38-39, 41-48; E.  
 A:Accession: S32597  
 A>Title: DNA sequence analysis of a 10.4 kbp region on the right arm of yeast chromosome 10.  
 A:Reference number: S50393; MID:95176111; PMID:7871832  
 A:Molecule type: DNA  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Cross-references: GI:33833; NID:493588; PIND:AB059313.1; PID:049700  
 A:Notes: The nucleotide sequence was submitted to the EMBL data Library, June 1994  
 J. Mol. Biol. 234: 700-721, 1993  
 A>Title: Evolution of allosteric control in glycogen phosphorylase.  
 A:Reference number: S40427; MID:94076345; PMID:8254568  
 A:Molecule type: protein  
 A:Genet. Sequences: SDD:5006344; MIPS:YPR150W  
 A:Map position: 168  
 A:Superfamily: phosphorylase  
 F:2-302/Product: glycogen phosphorylase status experimental <SW>  
 F:31/Binding site: phosphate (thr) (covalent) status experimental  
 F:75/Binding site: pyridoxal phosphate (lys) (covalent) status experimental  
 Query Match 7.04; Score 93; DB 2: Length 902;  
 Best Local Similarity 24.6%; Pred. No. 8.8;  
 Matches 49; Conservative 25; Mismatches 75; Indels 46; Gaps 10;  
 Qy 45 VPSNPLK EYLMKNDKVALEENSPATSEFRRVLTYSLSL--TYINLSSDD 101  
 Db 41 IDYHPLKSLANKVQK-----KFNKAIDQDR-FIRVETLANSLYN--CDNA 90  
 Qy 102 ETMSNPFTTN-----KFFLYVLESIFPLCALNCSIPQCM 144  
 Db 91 ATAAASHS EYLMKNDKVALEENSPATSEFRRVLTYSLSL--TYINLSSDD 146  
 Qy 145 PEVNSKPLKLYNCSNCKGKNSIFKYMNDQPKLOCTLSNPFTNFSIII-- 202  
 Db 147 PEPMASKSK-----PEMKTGALDGLQFEDYQDQNGSLGSLGALAFYDS 199  
 Qy 203 --TCTPSSGHS--RRTAL 218  
 Db 200 MATRIELPAMGLATETGI 218  
 RESU07 15  
 C888 precursor - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Accession: S32596; MID:75146541; PMID:1092346  
 C:Accession: S32596; MID:75146541; PMID:1092346  
 R:Isozo. T.; Seto, A.  
 Immunogenetics 42: 217-228, 1995  
 A:Reference number: 146850  
 A:Accession: S32596; MID:75146541; PMID:1092346  
 A:Molecule type: mRNA  
 A:Cross-references: GI:049843; MID:9755096; PIND:BA08643.1; PID:0755097

C:Superfamily: B-lymphocyte restricted antigen B7  
 Query Match 7.04; Score 92.5; DB 2: Length 299;  
 Best Local Similarity 19.44; Pred. No. 2.4;  
 Matches 47; Conservative 18; Mismatches 70; Indels 87; Gaps 12;  
 Qy 46 NVPLGE---YLMKNDKVALEENSPATSEFRRVLTYSLSL--TYINLSSDD 101  
 Db 52 NSISDELAHRRITMKNQDQWYLSISQGVVYRPYFDDIINLSLMLALRSLG 111  
 Qy 102 EY-----EMSPHIDDKKFFLYVLESLSPT--LACA 132  
 Db 112 TTCVKNKNSFRHGHVYLSIRAPYFPTDI-----GHPPYKWRKCS 162  
 Qy 133 LTNGSIYQVQKIPENYSHGLNLSMCKBCKNKSIFYKMSGDLQKLOCTLSNP 192  
 Db 163 ASGG---PSP-----PLANKGDCGLANLVY---DQDLYVLSVSEL 203  
 Qy 193 LPMYTS--SLITTTCTPSSG-----SRH-----YALIPFLAVITTCIV 231  
 Db 204 DEYTNMNSIV--GLIYKVELSCLFVNSKQDPTDGLPFWIIPGALVATVY 260  
 Qy 232 LV 233  
 Db 261 LV 262  
 Search completed: January 28, 2003, 08:40:50  
 Job Time : 16.9816 secs





GenCore version 3.1.3

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ON protein - protein search, using sw model

Run On: January 28, 2003, 08:38:45 : search time 16.3317 Seconds  
 634.907 MILLION cell updates/sec  
 (without alignments)

Title: US-09-730-465-2

Perfect score: 1376

Sequence: 1 WMSAGSAGSWSVCLL.....VLMGGLGCGPFRNSH 250

Scoring table: BLOSSUM62

Gap: 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum Match 10%

Listing first 45 summaries

Database : SwissProt.40\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1326	100.0	230	1	P19256 homo sapien
2	131.5	9.9	240	1	P18181 mus musc
3	126.5	9.5	247	1	P37598 equus cabal
4	126.5	9.5	247	1	P37598 equus cabal
5	115.5	8.7	331	1	P06729 homo sapien
6	113.5	8.5	655	1	G08477 homo sapien
7	105.5	8.0	773	1	P01932 cryotolagus
8	105.5	8.0	773	1	P01932 cryotolagus
9	103.7	7.8	240	1	P10232 rattus norv
10	86.5	6.7	306	1	P22770 mus muscu
11	92.5	7.0	239	1	P22770 mus muscu
12	91.5	6.9	634	1	P02470 mus muscu
13	91.5	6.9	634	1	P02470 mus muscu
14	89.5	6.7	873	1	P02470 mus muscu
15	89.5	6.7	873	1	P02470 mus muscu
16	88.5	6.7	306	1	P22770 mus muscu
17	88.5	6.7	306	1	P22770 mus muscu
18	87.5	6.6	281	1	P35811 homo sapien
19	87.5	6.6	281	1	P35811 homo sapien
20	86.5	6.6	901	1	P19256 homo sapien
21	85.5	6.4	526	1	P19256 homo sapien
22	85.5	6.4	757	1	P19256 homo sapien
23	85.5	6.4	757	1	P19256 homo sapien
24	85.5	6.4	757	1	P19256 homo sapien
25	85.5	6.4	757	1	P19256 homo sapien
26	85.5	6.4	757	1	P19256 homo sapien
27	85.5	6.4	757	1	P19256 homo sapien
28	85.5	6.4	757	1	P19256 homo sapien
29	84.5	6.3	310	1	P19256 homo sapien
30	84.5	6.3	310	1	P19256 homo sapien
31	84.5	6.3	310	1	P19256 homo sapien
32	84.5	6.3	310	1	P19256 homo sapien
33	83.5	6.3	1020	1	P19256 homo sapien

## ALIGNMENTS

RESULT 1	34	82.5	6.2	240	1	WFO_BAT
1	35	82.5	6.1	1018	1	CONT_BAT
2	36	81.5	6.1	880	1	U552_HSVGU
3	37	81.5	6.1	1484	1	U552_HSVGU
4	38	81.5	6.1	1484	1	U552_HSVGU
5	39	81.5	6.1	873	1	LOVE_BABET
6	40	81.5	6.1	873	1	LOVE_BABET
7	41	81.5	6.1	873	1	LOVE_BABET
8	42	81.5	6.1	873	1	LOVE_BABET
9	43	81.5	6.1	873	1	LOVE_BABET
10	44	81.5	6.1	873	1	LOVE_BABET
11	45	81.5	6.1	873	1	LOVE_BABET
12	46	81.5	6.1	873	1	LOVE_BABET
13	47	81.5	6.1	873	1	LOVE_BABET
14	48	81.5	6.1	873	1	LOVE_BABET
15	49	81.5	6.1	873	1	LOVE_BABET
16	50	81.5	6.1	873	1	LOVE_BABET
17	51	81.5	6.1	873	1	LOVE_BABET
18	52	81.5	6.1	873	1	LOVE_BABET
19	53	81.5	6.1	873	1	LOVE_BABET
20	54	81.5	6.1	873	1	LOVE_BABET
21	55	81.5	6.1	873	1	LOVE_BABET
22	56	81.5	6.1	873	1	LOVE_BABET
23	57	81.5	6.1	873	1	LOVE_BABET
24	58	81.5	6.1	873	1	LOVE_BABET
25	59	81.5	6.1	873	1	LOVE_BABET
26	60	81.5	6.1	873	1	LOVE_BABET
27	61	81.5	6.1	873	1	LOVE_BABET
28	62	81.5	6.1	873	1	LOVE_BABET
29	63	81.5	6.1	873	1	LOVE_BABET
30	64	81.5	6.1	873	1	LOVE_BABET
31	65	81.5	6.1	873	1	LOVE_BABET
32	66	81.5	6.1	873	1	LOVE_BABET
33	67	81.5	6.1	873	1	LOVE_BABET
34	68	81.5	6.1	873	1	LOVE_BABET
35	69	81.5	6.1	873	1	LOVE_BABET
36	70	81.5	6.1	873	1	LOVE_BABET
37	71	81.5	6.1	873	1	LOVE_BABET
38	72	81.5	6.1	873	1	LOVE_BABET
39	73	81.5	6.1	873	1	LOVE_BABET
40	74	81.5	6.1	873	1	LOVE_BABET
41	75	81.5	6.1	873	1	LOVE_BABET
42	76	81.5	6.1	873	1	LOVE_BABET
43	77	81.5	6.1	873	1	LOVE_BABET
44	78	81.5	6.1	873	1	LOVE_BABET
45	79	81.5	6.1	873	1	LOVE_BABET
46	80	81.5	6.1	873	1	LOVE_BABET
47	81	81.5	6.1	873	1	LOVE_BABET
48	82	81.5	6.1	873	1	LOVE_BABET
49	83	81.5	6.1	873	1	LOVE_BABET
50	84	81.5	6.1	873	1	LOVE_BABET
51	85	81.5	6.1	873	1	LOVE_BABET
52	86	81.5	6.1	873	1	LOVE_BABET
53	87	81.5	6.1	873	1	LOVE_BABET
54	88	81.5	6.1	873	1	LOVE_BABET
55	89	81.5	6.1	873	1	LOVE_BABET
56	90	81.5	6.1	873	1	LOVE_BABET
57	91	81.5	6.1	873	1	LOVE_BABET
58	92	81.5	6.1	873	1	LOVE_BABET
59	93	81.5	6.1	873	1	LOVE_BABET
60	94	81.5	6.1	873	1	LOVE_BABET
61	95	81.5	6.1	873	1	LOVE_BABET
62	96	81.5	6.1	873	1	LOVE_BABET
63	97	81.5	6.1	873	1	LOVE_BABET
64	98	81.5	6.1	873	1	LOVE_BABET
65	99	81.5	6.1	873	1	LOVE_BABET
66	100	81.5	6.1	873	1	LOVE_BABET
67	101	81.5	6.1	873	1	LOVE_BABET
68	102	81.5	6.1	873	1	LOVE_BABET
69	103	81.5	6.1	873	1	LOVE_BABET
70	104	81.5	6.1	873	1	LOVE_BABET
71	105	81.5	6.1	873	1	LOVE_BABET
72	106	81.5	6.1	873	1	LOVE_BABET
73	107	81.5	6.1	873	1	LOVE_BABET
74	108	81.5	6.1	873	1	LOVE_BABET
75	109	81.5	6.1	873	1	LOVE_BABET
76	110	81.5	6.1	873	1	LOVE_BABET
77	111	81.5	6.1	873	1	LOVE_BABET
78	112	81.5	6.1	873	1	LOVE_BABET
79	113	81.5	6.1	873	1	LOVE_BABET
80	114	81.5	6.1	873	1	LOVE_BABET
81	115	81.5	6.1	873	1	LOVE_BABET
82	116	81.5	6.1	873	1	LOVE_BABET
83	117	81.5	6.1	873	1	LOVE_BABET
84	118	81.5	6.1	873	1	LOVE_BABET
85	119	81.5	6.1	873	1	LOVE_BABET
86	120	81.5	6.1	873	1	LOVE_BABET
87	121	81.5	6.1	873	1	LOVE_BABET
88	122	81.5	6.1	873	1	LOVE_BABET
89	123	81.5	6.1	873	1	LOVE_BABET
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91	125	81.5	6.1	873	1	LOVE_BABET
92	126	81.5	6.1	873	1	LOVE_BABET
93	127	81.5	6.1	873	1	LOVE_BABET
94	128	81.5	6.1	873	1	LOVE_BABET
95	129	81.5	6.1	873	1	LOVE_BABET
96	130	81.5	6.1	873	1	LOVE_BABET
97	131	81.5	6.1	873	1	LOVE_BABET
98	132	81.5	6.1	873	1	LOVE_BABET
99	133	81.5	6.1	873	1	LOVE_BABET
100	134	81.5	6.1	873	1	LOVE_BABET
101	135	81.5	6.1	873	1	LOVE_BABET
102	136	81.5	6.1	873	1	LOVE_BABET
103	137	81.5	6.1	873	1	LOVE_BABET
104	138	81.5	6.1	873	1	LOVE_BABET
105	139	81.5	6.1	873	1	LOVE_BABET
106	140	81.5	6.1	873	1	LOVE_BABET
107	141	81.5	6.1	873	1	LOVE_BABET
108	142	81.5	6.1	873	1	LOVE_BABET
109	143	81.5	6.1	873	1	LOVE_BABET
110	144	81.5	6.1	873	1	LOVE_BABET
111	145	81.5	6.1	873	1	LOVE_BABET
112	146	81.5	6.1	873	1	LOVE_BABET
113	147	81.5	6.1	873	1	LOVE_BABET
114	148	81.5	6.1	873	1	LOVE_BABET
115	149	81.5	6.1	873	1	LOVE_BABET
116	150	81.5	6.1	873	1	LOVE_BABET
117	151	81.5	6.1	873	1	LOVE_BABET
118	152	81.5	6.1	873	1	LOVE_BABET
119	153	81.5	6.1	873	1	LOVE_BABET
120	154	81.5	6.1	873	1	LOVE_BABET
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122	156	81.5	6.1	873	1	LOVE_BABET
123	157	81.5	6.1	873	1	LOVE_BABET
124	158	81.5	6.1	873	1	LOVE_BABET
125	159	81.5	6.1	873	1	LOVE_BABET
126	160	81.5	6.1	873	1	LOVE_BABET
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134	168	81.5	6.1	873	1	LOVE_BABET
135	169	81.5	6.1	873	1	LOVE_BABET
136	170	81.5	6.1	873	1	LOVE_BABET
137	171	81.5	6.1	873	1	LOVE_BABET
138	172	81.5	6.1	873	1	LOVE_BABET
139	173	81.5	6.1	873	1	LOVE_BABET
140	174	81.5	6.1	873	1	LOVE_BABET
141	175	81.5	6.1	873	1	LOVE_BABET
142	176	81.5	6.1	873	1	LOVE_BABET
143	177	81.5	6.1	873	1	LOVE_BABET
144	178	81.5	6.1	873	1	LOVE_BABET
145	179	81.5	6.1	873	1	LOVE_BABET
146	180	81.5	6.1	873	1	LOVE_BABET
147	181	81.5	6.1	873	1	LOVE_BABET
148	182	81.5	6.1	873	1	LOVE_BABET
149	183	81.5	6.1	873	1	LOVE_BABET
150	184	81.5	6.1	873	1	LOVE_BABET
151	185	81.5	6.1	873	1	LOVE_BABET
152	186	81.5	6.1	873	1	LOVE_BABET
153	187	81.5	6.1	873	1	LOVE_BABET
154	188	81.5	6.1	873	1	LOVE_BABET
155	189	81.5	6.1	873	1	LOVE_BABET
156	190	81.5	6.1	873	1	LOVE_BABET
157	191	81.5	6.1	873	1	LOVE_BABET
158	192	81.5	6.1	873	1	LOVE_BABET
159	193	81.5	6.1	873	1	LOVE_BABET
160	194	81.5	6.1	873	1	LOVE_BABET
161	195	81.5	6.1	873	1	LOVE_BABET
162	196	81.5	6.1	873	1	LOVE_BABET
163	197	81.5	6.1	873	1	LOVE_BABET
164	198	81.5	6.1	873	1	LOVE_BABET
165	199	81.5	6.1	873	1	LOVE_BABET
166	200	81.5	6.1	873	1	LOVE_BABET
167	201	81.5	6.1	873	1	LOVE_BABET
168	202	81.5	6.1	873	1	LOVE_BABET
169	203	81.5	6.1	873	1	LOVE_BABET
170	204	81.5	6.1	873	1	LOVE_BABET
171	205	81.5	6.1	873	1	LOVE_BABET
172	206	81.5	6.1	873	1	LOVE_BABET
173	207	81.5	6.1	873	1	LOVE_BABET
174	208	81.5	6.1	873	1	LOVE_BABET
175	209	81.5	6.1	873	1	LOVE_BABET
176	210	81.5	6.1	873	1	LOVE_BABET
177	211	81.5	6.1	873	1	LOVE_BABET
178	212	81.5	6.1	873	1	LOVE_BABET
179	213	81.5	6.1	873	1	LOVE_BABET
180	214	81.5	6.1	873	1	LOVE_BABET
181	215	81.5	6.1	873	1	LOVE_BABET
182	216	81.5	6.1	873	1	LOVE_BABET
183	217	81.5	6.1	873	1	LOVE_BABET
184	218	81.5	6.1	873	1	LOVE_BABET
185	219	81.5	6.1	873	1	LOVE_BABET
186	220	81.5	6.1	873	1	LOVE_BABET
187	221	81.5	6.1	873	1	LOVE_BABET
188	222	81.5	6.1	873	1	LOVE_BABET
189	223	81.5	6.1	873	1	LOVE_BABET
190	224	81.5	6.1	873	1	LOVE_BABET
191	225	81.5	6.1	873	1	LOVE_BABET
192	226	81.5	6.1	873	1	LOVE_BABET
193	227	81.5	6.1	873	1	LOVE_BABET
194	228	81.5	6.1	873	1	LOVE_BABET
195	229	81.5	6.1	873	1	LOVE_BABET
196	230	81.5	6.1	873	1	LOVE_BABET
197	231	81.5	6.1	873	1	LOVE_BABET
198	232	81.5	6.1	873	1	LOVE_BABET
199	233	81.5	6.1	873	1	LOVE_BABET
200	234	81.5	6.1	873	1	LOVE_BABET
201	235	81.5	6.1	873	1	LOVE_BABET
202	236	81.5	6.1	873	1	LOVE_BABET
203	237	81.5	6.1	873	1	LOVE_BABET
204	238	81.5	6.1	873	1	LOVE_BABET
205	239	81.5	6.1	873		











































Genome version 5.1.3

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OM protein - protein search, using sw model

Run on: January 28, 2003, 08:38:45

Search time 18.0184 Seconds  
(without alignments)  
393,363 Million cell updates/sec

Title: US-09-730-465-8

Sequence: 1 WAGSAGRALQVSVCL.....MREALNNVYQSLSGPK 347

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 283224 seqs, 9613442 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100

Listing first 45 summaries

Database: 1: Pfam1

2: Pfam2

3: Pfam3

4: Pfam4

5: Pfam5

6: Pfam6

7: Pfam7

8: Pfam8

9: Pfam9

10: Pfam10

11: Pfam11

12: Pfam12

13: Pfam13

14: Pfam14

15: Pfam15

16: Pfam16

17: Pfam17

18: Pfam18

19: Pfam19

20: Pfam20

21: Pfam21

22: Pfam22

23: Pfam23

24: Pfam24

25: Pfam25

26: Pfam26

27: Pfam27

28: Pfam28

29: Pfam29

30: Pfam30

31: Pfam31

32: Pfam32

33: Pfam33

34: Pfam34

35: Pfam35

36: Pfam36

37: Pfam37

38: Pfam38

39: Pfam39

40: Pfam40

41: Pfam41

42: Pfam42

43: Pfam43

44: Pfam44

45: Pfam45

46: Pfam46

47: Pfam47

48: Pfam48

49: Pfam49

50: Pfam50

51: Pfam51

52: Pfam52

53: Pfam53

Result	Score	Match	Length	DB	ID	Description
1	1233	66.4	255	4	S31866	Ig gamma-1 chain C
2	1223	66.4	330	1	GMS9	Ig gamma-1 chain C
3	1223	66.4	330	1	GMS9	Ig gamma-1 chain C
4	1160	63.6	234	2	PF0207	Ig gamma chain C
5	1146	61.7	377	2	A23511	Ig gamma-3 chain C
6	1146	61.7	377	2	A23511	Ig gamma-3 chain C
7	1144	61.6	377	2	A60764	Ig gamma-3 chain C
8	1135	61.2	327	1	G4897	Ig gamma-4 chain C
9	1135	61.2	327	1	G4897	Ig gamma-4 chain C
10	926.5	49.3	323	1	GMS9	Ig gamma heavy chain
11	913.5	49.2	328	2	I47160	Ig gamma-2b chain
12	913.5	49.2	328	2	I47160	Ig gamma-2b chain
13	906.5	48.0	277	2	I47162	Ig gamma-2b chain
14	894.5	48.2	328	2	I47158	Ig gamma-1 chain C
15	894.5	48.2	328	2	I47158	Ig gamma-1 chain C
16	887.5	48.0	328	1	G259	Ig gamma-2 chain C
17	857.5	46.2	470	2	S22080	Ig heavy chain pre
18	846.5	45.6	308	2	C30554	Ig heavy chain C
19	846.5	45.6	308	2	C30554	Ig heavy chain C
20	845.5	45.6	331	1	G3N82	Ig gamma-1 chain C
21	838.5	45.2	332	2	P50018	Ig gamma-2b chain
22	838.5	45.2	332	2	P50018	Ig gamma-2b chain
23	829.5	44.0	498	2	GMS9	Ig gamma-3 chain C
24	829.5	44.0	498	2	GMS9	Ig gamma-3 chain C
25	819.5	44.1	336	2	P50017	Ig gamma-1 chain C
26	818.5	43.8	334	1	G1M5	Ig gamma-1 chain C
27	812.5	43.1	329	2	S00847	Ig gamma-2b chain
28	811.5	43.7	330	1	G2N84	Ig gamma-2b chain
29	811.5	43.7	469	2	S37483	Ig gamma-2b chain

Prod. No. is the number of results predicted by chance to have a  
match of this quality or better. The results are sorted by prod. no.  
and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

## RESULT 1

S31866

Ig gamma-1 chain C region - synthetic

CSpecies: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

Accession: S31866

Accession: S31866

Accession: S31866

Accession: S31866

Accession: S31866

Accession: S31866

Accession: S31866

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Accession: S31866



















1. MOLECULAR TYPE: protein  
US-07-940-861-10

Query Match Similarity 100.0% Score 1376; DB 1; Length 250;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 60  
DB 1 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 60  
OY 61 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 120  
DB 61 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 120  
OY 121 LESLSPFTLCALNGSIEVQCHPEYVNSHGLINWSDCMQCKRNSITVFMKND 180  
DB 121 LESLSPFTLCALNGSIEVQCHPEYVNSHGLINWSDCMQCKRNSITVFMKND 180  
OY 181 LKQICTGSLNPLNTSSITLTCTPSSGSHNRHALPIPLAVITCTVYVNMGLAC 240  
DB 181 LKQICTGSLNPLNTSSITLTCTPSSGSHNRHALPIPLAVITCTVYVNMGLAC 240  
OY 241 DRKDFPTNSN 250  
DB 241 DRKDFPTNSN 250

## RESULT 2

US-08-459-512-10  
Patent No. 5914111

GENERAL INFORMATION: INC

APPLICANT: BLOOM, INC.

APPLICANT: MILLER, Glenn T.

APPLICANT: MILLER, Glenn T.

TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3

NUMBER OF SEQUENCES: 43

ADDRESS: Fish & Neave

STREET: 875 Third Avenue

CITY: New York

COUNTRY: U.S.A.

ZIP: 10022-6250

COMPUTER TYPE: IBM PC compatible

SOFTWARE: IBM PC compatible

CURRENT APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

CLASSIFICATION: 514

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

SEQUENCE CHARACTERISTICS  
US-08-459-512-10  
TYPE: amino acid  
MOLECULAR TYPE: protein  
US-08-459-512-10

Query Match 100.0% Score 1376; DB 1; Length 250;  
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 60  
DB 1 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 60  
OY 61 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 120  
DB 61 MYAGSNGRAGLGVSVCLACGRTSCFSQIYGVYGVNTHPNSVPLAEVLMKKQ 120  
OY 121 LESLSPFTLCALNGSIEVQCHPEYVNSHGLINWSDCMQCKRNSITVFMKND 180  
DB 121 LESLSPFTLCALNGSIEVQCHPEYVNSHGLINWSDCMQCKRNSITVFMKND 180  
OY 181 LKQICTGSLNPLNTSSITLTCTPSSGSHNRHALPIPLAVITCTVYVNMGLAC 240  
DB 181 LKQICTGSLNPLNTSSITLTCTPSSGSHNRHALPIPLAVITCTVYVNMGLAC 240  
OY 241 DRKDFPTNSN 250  
DB 241 DRKDFPTNSN 250

## RESULT 3

US-08-459-457-10

Patent No. 5914111

GENERAL INFORMATION: INC

APPLICANT: BLOOM, INC.

APPLICANT: MILLER, Glenn T.

APPLICANT: MILLER, Glenn T.

TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3

NUMBER OF SEQUENCES: 43

ADDRESS: Fish & Neave

STREET: 875 Third Avenue

CITY: New York

COUNTRY: U.S.A.

ZIP: 10022-6250

COMPUTER TYPE: IBM PC compatible

SOFTWARE: IBM PC compatible

CURRENT APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

CLASSIFICATION: 514

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

PRIOR APPLICATION DATA: PCT/US92/02050

APPLICATION NUMBER: US 07/770,967

FILED DATE: 12-MAR-1992

TELEPHONE: (212)715-0600  
 TELEFAX: (212)715-0673  
 TELEFAX: 14-8567  
 INFORMATION ID NO.: 10;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 250 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 100.0%; Score 1346; Db 2; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 1.7E-126;  
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYASDGRALGVSVCLLRKQPICTSCSQITGVYGVNTTFVSPNPLKYLAKKQK 60  
 Db 1 MYASDGRALGVSVCLLRKQPICTSCSQITGVYGVNTTFVSPNPLKYLAKKQK 60  
 Qy 61 DVALENSFPAFSPFNKAYLDVYSGSLTTLVYSSDEEDYDMSPTDTMKFLV 120  
 Db 61 DVALENSFPAFSPFNKAYLDVYSGSLTTLVYSSDEEDYDMSPTDTMKFLV 120  
 Qy 121 LESLSPLTLCALNSIEVQCMIPFNHSHGLIWSNCPMCKKNSSTIFEMND 180  
 Db 121 LESLSPLTLCALNSIEVQCMIPFNHSHGLIWSNCPMCKKNSSTIFEMND 180  
 Qy 181 LQKIOCTLSNPFTSILLTCTPSGSRHRVYALPIPLAVTTCVLMNGILAC 240  
 Db 181 LQKIOCTLSNPFTSILLTCTPSGSRHRVYALPIPLAVTTCVLMNGILAC 240  
 Qy 241 DKDFQRTNSN 250  
 Db 241 DKDFQRTNSN 250

RESULT 4  
 US-08-460-132-10

Sequence 10, Application US/08460132  
 GENERAL INFORMATION:  
 APPLICANT: BIOGEN, INC., Boston, Massachusetts P.  
 APPLICANT: MILLER, Glenn T.  
 APPLICANT: ROSA, Margaret D.  
 TITLE OF INVENTION: FUNCTION ASSOCIATED WITH  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 STREET: 975 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10022-6250

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/460,132  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 FILING DATE: 21-OCT-1992  
 FILING DATE: 12-MAR-1992  
 APPLICATION NUMBER: US 07/667,971  
 FILING DATE: 12-MAR-1991  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/770,967  
 FILING DATE: 07-OCT-1991  
 APPLICANT: BIOGEN, INC., Boston, Massachusetts P.  
 APPLICANT: MILLER, Glenn T.  
 APPLICANT: ROSA, Margaret D.  
 TITLE OF INVENTION: FUNCTION ASSOCIATED WITH  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 STREET: 975 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10022-6250

Query Match 100.0%; Score 1346; Db 2; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 1.7E-126;  
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYASDGRALGVSVCLLRKQPICTSCSQITGVYGVNTTFVSPNPLKYLAKKQK 60  
 Db 1 MYASDGRALGVSVCLLRKQPICTSCSQITGVYGVNTTFVSPNPLKYLAKKQK 60  
 Qy 61 DVALENSFPAFSPFNKAYLDVYSGSLTTLVYSSDEEDYDMSPTDTMKFLV 120  
 Db 61 DVALENSFPAFSPFNKAYLDVYSGSLTTLVYSSDEEDYDMSPTDTMKFLV 120  
 Qy 121 LESLSPLTLCALNSIEVQCMIPFNHSHGLIWSNCPMCKKNSSTIFEMND 180  
 Db 121 LESLSPLTLCALNSIEVQCMIPFNHSHGLIWSNCPMCKKNSSTIFEMND 180  
 Qy 181 LQKIOCTLSNPFTSILLTCTPSGSRHRVYALPIPLAVTTCVLMNGILAC 240  
 Db 181 LQKIOCTLSNPFTSILLTCTPSGSRHRVYALPIPLAVTTCVLMNGILAC 240  
 Qy 241 DKDFQRTNSN 250  
 Db 241 DKDFQRTNSN 250

RESULT 5

US-08-466-465-2  
 Sequence 10, Application US/08466465  
 GENERAL INFORMATION:  
 APPLICANT: BIOGEN, INC., Boston, Massachusetts P.  
 APPLICANT: MILLER, Glenn T.  
 APPLICANT: ROSA, Margaret D.  
 TITLE OF INVENTION: FUNCTION ASSOCIATED WITH  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 STREET: 975 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10022-6250

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,465  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 FILING DATE: 21-OCT-1992  
 FILING DATE: 12-MAR-1992  
 APPLICATION NUMBER: US 07/667,971  
 FILING DATE: 12-MAR-1991  
 PRIOR APPLICATION DATA:

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,465  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 FILING DATE: 21-OCT-1992  
 FILING DATE: 12-MAR-1992  
 APPLICATION NUMBER: US 07/667,971  
 FILING DATE: 12-MAR-1991  
 PRIOR APPLICATION DATA:

1 APPLICATION NUMBER: US 07/862,022  
 2 FILING DATE: 12-APR-1992  
 3 PUBLICATION DATE: 07-APR-1992  
 4 APPLICATION NUMBER: US 07/770,969  
 5 FILING DATE: 07-OCT-1991  
 6 INVENTOR: HALEY, James P. Jr.  
 7 NAME: HALEY, James P. Jr.  
 8 REGISTRATION NUMBER: 35,964  
 9 TELEPHONE: (617)227-4941  
 10 TELECOMMUNICATION INFORMATION: 51C1P2  
 11 TELEFAX: (617)227-7400  
 12 INVOICE: 617227-4941  
 13 NUMBER OF SEQUENCES: 2  
 14 SEQUENCE CHARACTERISTICS:  
 15 LENGTH: 250 amino acids  
 16 MOLECULE TYPE: protein  
 17 TOPOLOGY: linear  
 18 US-08-466-485-2

Query Match 100.0% Score 1326; DB 4; Length 250;  
 Best Local Similarity 100.0% Pct Ident 100.0%  
 Matches 250; Conservative 0; Mismatches 0; Gaps 0;  
 QY 1 WAGSDAGRALGVSLVCLLCGCTGFCFSQOITGVYGVTHFVSNPLAEVLAHKQK 60  
 DB 1 WAGSDAGRALGVSLVCLLCGCTGFCFSQOITGVYGVTHFVSNPLAEVLAHKQK 60  
 QY 61 DYVAELNRFASFNNRVLYDVSGLTITNLTSSDDRYEMSPITDMKFFLY 120  
 DB 61 DYVAELNRFASFNNRVLYDVSGLTITNLTSSDDRYEMSPITDMKFFLY 120  
 QY 121 LESLPSPTLCALNLSIVQCNPEHNSHRLGLINSMQCMQCKNSTSYFKNND 180  
 DB 121 LESLPSPTLCALNLSIVQCNPEHNSHRLGLINSMQCMQCKNSTSYFKNND 180  
 QY 181 LPKIOCTLSNLFMTSSILTCIPSGSHRHVALIPIPLAVITTCIVYMWGLK 240  
 DB 181 LPKIOCTLSNLFMTSSILTCIPSGSHRHVALIPIPLAVITTCIVYMWGLK 240  
 QY 241 DRKFOPTNSN 250  
 DB 241 DRKFOPTNSN 250

RESULT 6  
 1 PCT-US92-02050-10  
 2 GENERAL INFORMATION: PCT/US9202050

1 APPLICANT: BIONE, INC. bcs p.  
 2 APPLICANT: MILLER, Glenn T.  
 3 APPLICANT: ROSA, Margaret D.  
 4 TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3  
 5 NUMBER OF SEQUENCES: 43  
 6 COMPLETION DATE: 10-APR-1985  
 7 ADDRESS: Fish & Neave  
 8 STREET: 875 Third Avenue  
 9 CITY: New York  
 10 STATE: NY  
 11 COUNTRY: U.S.A.  
 12 ZIP: 10022-6250  
 13 QUERY: 0022-6250  
 14 MEDIUM TYPE: Floppy disk  
 15 COMMENT: IBM PC compatible DOS  
 16 SOFTWARE: PatentIn Release 1.0, Version #1.25  
 17 CURRENT APPLICATION DATA:  
 18 PCT NUMBER: PCT/US92/02050  
 19 FILING DATE: 19920312  
 20 CLASSIFICATION: 435  
 21 PRIOR APPLICATION DATA:

1 APPLICATION NUMBER: US 07/667,971  
 2 FILING DATE: 12-MAR-1991  
 3 PUBLICATION DATE: 07-APR-1992  
 4 APPLICATION NUMBER: US 07/770,967  
 5 FILING DATE: 07-OCT-1991  
 6 INVENTOR: HALEY, James P. Jr.  
 7 NAME: HALEY, James P. Jr.  
 8 REGISTRATION NUMBER: 27,794  
 9 TELEPHONE: (617)227-4941  
 10 TELECOMMUNICATION INFORMATION: 51C1P2  
 11 TELEFAX: (617)227-7400  
 12 INFORMATION FOR SEQ ID NO: 10:  
 13 SEQUENCE CHARACTERISTICS:  
 14 LENGTH: 250 amino acids  
 15 MOLECULE TYPE: protein  
 16 TOPOLOGY: linear  
 17 US-08-466-485-2

Query Match 100.0% Score 1326; DB 5; Length 250;  
 Best Local Similarity 100.0% Pct Ident 100.0%  
 Matches 250; Conservative 0; Mismatches 0; Gaps 0;  
 QY 1 WAGSDAGRALGVSLVCLLCGCTGFCFSQOITGVYGVTHFVSNPLAEVLAHKQK 60  
 DB 1 WAGSDAGRALGVSLVCLLCGCTGFCFSQOITGVYGVTHFVSNPLAEVLAHKQK 60  
 QY 61 DYVAELNRFASFNNRVLYDVSGLTITNLTSSDDRYEMSPITDMKFFLY 120  
 DB 61 DYVAELNRFASFNNRVLYDVSGLTITNLTSSDDRYEMSPITDMKFFLY 120  
 QY 121 LESLPSPTLCALNLSIVQCNPEHNSHRLGLINSMQCMQCKNSTSYFKNND 180  
 DB 121 LESLPSPTLCALNLSIVQCNPEHNSHRLGLINSMQCMQCKNSTSYFKNND 180  
 QY 181 LPKIOCTLSNLFMTSSILTCIPSGSHRHVALIPIPLAVITTCIVYMWGLK 240  
 DB 181 LPKIOCTLSNLFMTSSILTCIPSGSHRHVALIPIPLAVITTCIVYMWGLK 240  
 QY 241 DRKFOPTNSN 250  
 DB 241 DRKFOPTNSN 250

RESULT 7  
 1 PCT-US92-02050-10  
 2 GENERAL INFORMATION: PCT/US9202050  
 3 APPLICANT: BIONE, INC. bcs p.  
 4 APPLICANT: MILLER, BARBARA  
 5 APPLICANT: ROSA, Margaret D.  
 6 TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3  
 7 NUMBER OF SEQUENCES: 43  
 8 COMPLETION DATE: 10-APR-1985  
 9 ADDRESS: Fish & Neave  
 10 STREET: 875 Third Avenue  
 11 CITY: New York  
 12 STATE: NY  
 13 COUNTRY: U.S.A.  
 14 ZIP: 10022-6250  
 15 QUERY: 0022-6250  
 16 MEDIUM TYPE: Floppy disk  
 17 COMMENT: IBM PC compatible DOS  
 18 SOFTWARE: PatentIn Release 1.0, Version #1.25  
 19 CURRENT APPLICATION DATA:  
 20 PCT NUMBER: PCT/US92/02050  
 21 FILING DATE: 19920312  
 22 CLASSIFICATION: 435  
 23 PRIOR APPLICATION DATA:

Query Match 100.0% Score 1326; DB 6; Length 250;  
 Best Local Similarity 100.0% Pct Ident 100.0%  
 Matches 250; Conservative 0; Mismatches 0; Gaps 0;  
 QY 1 WAGSDAGRALGVSLVCLLCGCTGFCFSQOITGVYGVTHFVSNPLAEVLAHKQK 60  
 DB 1 WAGSDAGRALGVSLVCLLCGCTGFCFSQOITGVYGVTHFVSNPLAEVLAHKQK 60  
 QY 61 DYVAELNRFASFNNRVLYDVSGLTITNLTSSDDRYEMSPITDMKFFLY 120  
 DB 61 DYVAELNRFASFNNRVLYDVSGLTITNLTSSDDRYEMSPITDMKFFLY 120









COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

FILE NAME: 020501.DAT

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent InRelease 11.0, Version 1.0

APPLICANT NUMBER: US/US92/02050

APPLICATION NUMBER: 19203012

FILING DATE: 19920312

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07667, 971

PRIOR APPLICATION NUMBER: US 07667, 971

PRIOR APPLICATION DATA: US 07770, 967

ATTORNEY/AGENCY INFORMATION:

NAME: BARRY W. HANSEN

NAME: BARRY W. HANSEN

ADDRESS: 27, 754

REFERENCE/DOCKET NUMBER: 81531CF2

TELEPHONE/COMMUNICATION INFORMATION:

TELEPHONE: 212-715-1673

TELEFAX: 212-715-1673

TELETYPE: 212-715-1673

INFORMATION FOR SEQ ID NO: 12:

TYPE: Amino acid sequence

TYPE: Amino acid sequence

TOPOLOGY: linear

LOCUS: 1982020501.DAT

GenCore version 5.1.3  
Copyright (C) 1993 - 2003 CompuLink Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2003, 08:40:59 ; Search time 82.077 Seconds  
(without alignments)  
61,662 Million cell updates/sec

Title: us-09-730-465-2

Score: 1

Sequences: 1 MWASDRAHGVSWCLL.....VLNNKILCKDRKDFNSN 250

Scoring table:

Gap: 10.0 , Gapext 0.5

Searched: 12226 seqs, 2078551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 0%

Listing first 45 summaries

Database: 1 Published Applications, 34  
2: /cgn2\_5/p/odata2/pubseq/US08\_NMK\_PUB pep.\*  
3: /cgn2\_5/p/odata2/pubseq/US08\_NMK\_PUB pep.\*  
4: /cgn2\_5/p/odata2/pubseq/US08\_NMK\_PUB pep.\*  
5: /cgn2\_5/p/odata2/pubseq/US07\_NMK\_PUB pep.\*  
6: /cgn2\_5/p/odata2/pubseq/US07\_PUSCMB pep.\*  
7: /cgn2\_5/p/odata2/pubseq/US08\_PUSCMB pep.\*  
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11: /cgn2\_5/p/odata2/pubseq/US10\_NMK\_PUB pep.\*  
12: /cgn2\_5/p/odata2/pubseq/US10\_PUSCMB pep.\*  
13: /cgn2\_5/p/odata2/pubseq/US10\_NMK\_PUB pep.\*  
14: /cgn2\_5/p/odata2/pubseq/US08\_PUSCMB pep.\*

Pred. No. is the number of results predicted by chance to have a  
minimum match of the specified length. The results are sorted  
and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query Match	Length	DB ID	Description
1	1326	100.0	250	10 US-05-796-033-2	Sequence 2, Appl
2	1326	100.0	250	10 US-05-730-465-2	Sequence 2, Appl
3	1230	94.3	240	10 US-05-730-465-4	Sequence 4, Appl
4	1230	94.3	240	10 US-05-730-465-4	Sequence 4, Appl
5	630	47.5	347	9 US-10-091-26-17	Sequence 17, Appl
6	630	47.5	347	10 US-05-796-033-8	Sequence 8, Appl
7	630	47.5	347	10 US-05-796-033-8	Sequence 8, Appl
8	115.5	8.7	331	10 US-05-796-033-6	Sequence 6, Appl
9	115.5	8.7	331	10 US-05-730-465-6	Sequence 6, Appl
10	115.5	8.7	331	10 US-05-730-465-6	Sequence 6, Appl
11	105.5	8.0	773	10 US-05-816-247-6	Sequence 6, Appl
12	90	6.8	312	10 US-09-732-524-4	Sequence 4, Appl
13	90	6.8	335	9 US-09-989-259-253	Sequence 253, App
14	90	6.8	335	9 US-09-989-259-253	Sequence 253, App
15	90	6.8	335	9 US-10-063-547-46	Sequence 46, Appl
16	90	6.8	335	9 US-09-989-735-253	Sequence 253, App
17	90	6.8	335	9 US-09-989-735-253	Sequence 253, App
18	90	6.8	335	9 US-09-989-735-253	Sequence 253, App
19	90	6.8	335	9 US-09-990-436-253	Sequence 253, App

20	90	6.8	335	9 US-09-991-181-253	Sequence 253, App
21	90	6.8	335	9 US-09-991-181-253	Sequence 253, App
22	90	6.8	335	9 US-09-991-181-253	Sequence 253, App
23	90	6.8	335	9 US-09-991-181-253	Sequence 253, App
24	90	6.8	335	9 US-10-174-520-192	Sequence 192, App
25	90	6.8	335	9 US-10-174-520-192	Sequence 192, App
26	90	6.8	335	9 US-10-063-656-46	Sequence 46, Appl
27	90	6.8	335	9 US-10-063-656-46	Sequence 46, Appl
28	90	6.8	335	9 US-10-063-656-46	Sequence 46, Appl
29	90	6.8	335	9 US-10-063-656-46	Sequence 46, Appl
30	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
31	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
32	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
33	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
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35	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
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37	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
38	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
39	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
40	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
41	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
42	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
43	90	6.8	335	9 US-09-989-725-253	Sequence 253, App
44	88.5	6.7	306	10 US-09-871-867A-17	Sequence 17, Appl
45	88	6.6	313	10 US-09-756-985-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-09-796-033-2  
Sequence 2, Appl Application US/09796033  
Patent No. US2002009446A1  
GENERAL INFORMATION:  
TITLE OF INVENTION: METHOD OF MODULATING MEMORY EFFECTOR  
IN T-CELLS AND COMPOSITIONS  
INVENTOR: JAMES M. HARRIS, JR.  
CURRENT APPLICATION NUMBER: US/09796,033  
CURRENT FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: US/0599/20026  
PRIOR APPLICATION NUMBER: US/08-08-31  
PRIOR APPLICATION NUMBER: US/06/098,456  
PRIOR FILING DATE: 1998-08-31  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2  
US09796033.2  
TYPE: PPT  
ORGANISM: Homo sapiens  
FEATURE: SIGNAL  
LOCATION: (1)...(28)  
US-09-796-033-2

Query Match	100.0%	Score	1326;	DB	10;	Length	250;
Best Local Similarity	100.0%	Pred.	No. 2	6e-112;			
Matches	250;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Oy	1	MWASDRAHGVSWCLLGGFCFCQIGVGYNTFVFNPLVKKKKR	60				
Db	1	MWASDRAHGVSWCLLGGFCFCQIGVGYNTFVFNPLVKKKKR	60				
Oy	61	DAVLENSPFAFSSKNRKYLDVTSSSLTWTSSSEDETSNPDTDTMFLLV	120				
Db	61	DAVLENSPFAFSSKNRKYLDVTSSSLTWTSSSEDETSNPDTDTMFLLV	120				
Oy	131	LESLSPFLTALTNLSNQCMIPENYNSHGLNLSWCMQMDQRANSSTYTMND	160				
Db	131	LESLSPFLTALTNLSNQCMIPENYNSHGLNLSWCMQMDQRANSSTYTMND	160				

Qy 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGLKAC 240  
 Db 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGLKAC 240  
 Qy 241 DRKDFRTNSH 250  
 Db 241 DRKDFRTNSH 250

RESULT 2  
 US-09-730-465-2  
 : Sequence 2, Application US/09730465  
 : Patent No. US002009449A1  
 : GENERAL APPLICANT: Walinger, Barbara P.  
 : APPLICANT: Cooper, Kevin D.  
 : TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen  
 : Presenting Cell Driven Skin Conditions Using  
 : Inhibitors of the CD2/LEA-3 Interaction  
 : NUMBER OF SEQUENCES: 8  
 : CURRENT APPLICATION NUMBER: US/09730465  
 : ADDRESS: LANIVE & COCKFIELD  
 : STREET: 60 State Street, Suite 510  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: USA  
 : ZIP: 02109-1875  
 : TELEPHONE: 617-227-5941  
 : COMMUNICATION TYPE: Floppy disk  
 : COMPUTER: IBM PC Compatible  
 : SOFTWARE: IBM PC DOS  
 : SOFTWARE: Retain in Release 11.0, Version 11.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09730465  
 : PRIORITY APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/US92/08755  
 : FILING DATE: 12 APR-1992  
 : APPLICATION NUMBER: US 07/862,022  
 : FILING DATE: 12 APR-1992  
 : FILING DATE: 07-OCT-1991  
 : ATTORNEY/AGENT INFORMATION:  
 : REGISTRATION NUMBER: 135,965  
 : REFERENCE/DOCKET NUMBER: BSH-111CP  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 617-227-5941  
 : TELEFAX: (617)227-5941  
 : INFORMATION FOR SEQ ID NO. 2:  
 : SEQ ID NO. 2:  
 : LENGTH: 251 amino acids  
 : TYPE: amino acid  
 : MOLECULE TYPE: linear  
 : SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 : US-09-730-465-2

Query Match 100.0%; Score 1326; DB 10; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-112;  
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWGSDAGAGLVSVCLLCIGFSGFQVGYGVNTFVFNPNFLVLAHKKK 60  
 Db 1 MWGSDAGAGLVSVCLLCIGFSGFQVGYGVNTFVFNPNFLVLAHKKK 60  
 Qy 61 DYKALENSFPAFSSFNRYLYDTSSGSLTYNTSSDDDESMESPNITDTMKFLY 120  
 Db 61 DYKALENSFPAFSSFNRYLYDTSSGSLTYNTSSDDDESMESPNITDTMKFLY 120  
 Qy 121 LESLSPFTLCALTNWSIEVQCHPHNHSRGLMNSDCMPCMCNKSSTFTKMD 180  
 Db 121 LESLSPFTLCALTNWSIEVQCHPHNHSRGLMNSDCMPCMCNKSSTFTKMD 180  
 Qy 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGL 237  
 Db 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGL 237

Qy 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGLKAC 240  
 Db 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGLKAC 240  
 Qy 241 DRKDFRTNSH 250  
 Db 241 DRKDFRTNSH 250

RESULT 3  
 US-09-730-465-3  
 : Sequence 4, Application US/0976033  
 : Patent No. US002009449A1  
 : GENERAL APPLICANT: Walinger, Barbara P.  
 : APPLICANT: Magliav, Daniel  
 : TITLE OF INVENTION: METHOD OF MODULATING MEMORY EFFECTOR  
 : CELL ACTIVITY IN TISSUES AND COMPOSITIONS  
 : FILE REFERENCE: 10274-041001  
 : CURRENT APPLICATION NUMBER: US/0976033  
 : PRIORITY APPLICATION NUMBER: PCT/US99/20026  
 : PRIOR FILING DATE: 1999-08-31  
 : PRIOR APPLICATION NUMBER: US 60/098,456  
 : PRIOR FILING DATE: 1999-08-31  
 : NUMBER OF SEQ ID NOS: 8  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SERIAL NO.: 10274-041001  
 : LENGTH: 240  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : PHYNOM: HOMO  
 : NAME/KEY: SIGNAL  
 : LOCATION: (1)...(28)  
 : US-09-730-465-3

Query Match 94.3%; Score 1250; Length 240;  
 Best Local Similarity 94.3%; Pred. No. 2.6e-112;  
 Matches 236; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWGSDAGAGLVSVCLLCIGFSGFQVGYGVNTFVFNPNFLVLAHKKK 60  
 Db 1 MWGSDAGAGLVSVCLLCIGFSGFQVGYGVNTFVFNPNFLVLAHKKK 60  
 Qy 61 DYKALENSFPAFSSFNRYLYDTSSGSLTYNTSSDDDESMESPNITDTMKFLY 120  
 Db 61 DYKALENSFPAFSSFNRYLYDTSSGSLTYNTSSDDDESMESPNITDTMKFLY 120  
 Qy 121 LESLSPFTLCALTNWSIEVQCHPHNHSRGLMNSDCMPCMCNKSSTFTKMD 180  
 Db 121 LESLSPFTLCALTNWSIEVQCHPHNHSRGLMNSDCMPCMCNKSSTFTKMD 180  
 Qy 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGL 237  
 Db 181 LQKIOCTLQNPFTFSSILTCIPSSGSHRRHYALPIPLAVITCVIYMMGL 237

RESULT 4  
 US-09-730-465-4  
 : Sequence 4, Application US/09730465  
 : Patent No. US002009449A1  
 : GENERAL APPLICANT: Walinger, Barbara P.  
 : APPLICANT: Cooper, Kevin D.  
 : TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen  
 : Presenting Cell Driven Skin Conditions Using  
 : Inhibitors of the CD2/LEA-3 Interaction  
 : NUMBER OF SEQUENCES: 8  
 : CURRENT APPLICATION NUMBER: US/09730465  
 : ADDRESS: LANIVE & COCKFIELD  
 : STREET: 60 State Street, Suite 510  
 : CITY: Boston  
 : STATE: Massachusetts







STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

ZIP: 02109-1875

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Version 11.25

PRIOR APPLICATION DATA: PCT/US93/08755

FILING DATE: 06/02/1992

FILING DATE: 12/04/1992

ATTORNEY/AGENT INFORMATION: 91

NAME: Meets, Louis (PM)

REFERENCE/DOCKET NUMBER: BOP-111CP

TELEPHONE: (617) 227-7400

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-730-465-6

Query Match

Best Local Similarity 8.74; Score 115.5; DB 10; Length 351;

Matches 59; Conservative 42; Mismatches 76; Indels 79; Gaps

32 QIVGVYGVNTPVPS---SVPLKLVKQKVALENSFAPFSFKNVYLVVSS---S 89

Db 32 ETNGLAQINDLITPSQMSDIDQIDAMKTSIKKRIKAFKREKTKOTFLRN-- 89

Qy 82 YIVGSSGLNLTNITSDDETEY---ESNPITDMKFFLYLVLESPLF--- 127

Db 90 ---GKLAHKLQDQIDNIVSTGNGKVKLEI-FLLKIQVSKPKISWCINT 142

Qy 128 TLIALNNSITVCPHFP-----HYNSHRLGMLSNICDPECKCKNSTIYFNEN 179

Db 143 TLIVCVNMT-----DPLNLYIQGKHLKLSQVTHK-----TTS 179

Qy 180 DLPKQVQTLQNPVNTKRIITLFCFSQSHSRHVALDIP---PLAVITCVLM 234

Db 180 -LSNKFCTAGKY-SKESSVPSVC-PKNG-LDTLLIGCGGSLMFFVLLVPTI 234

Qy 235 NGLACDKRDPFNSN 250

Db 235 T-----KKKQNSRN 245

RESULT 10

Sequence 2, Application US/09882107

Patent No. US2002015958A1

GENERAL INFORMATION NUMBER C.

APPLICANT: HEIN, MICHAEL B.

TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING

ANTIBODIES TO PLANT PROTECTION PROTEINS IN PLANTS AND THEIR USE

FILE REFERENCE: EP130026

CURRENT APPLICATION NUMBER: US/09/982,107

CURRENT FILING DATE: 2001-10-16

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patent Ver. 2.1

SEQ ID NO: 73

TYPE: PRT

ORGANISM: Oryctolagus cuniculus

US-09-902-107-2

Query Match

Best Local Similarity 8.04; Score 105.5; DB 9; Length 773;

Matches 47; Conservative 39; Mismatches 79; Indels 49; Gaps

39 GNVTWP-----SVPLKLVKQKVALENSFAPFSFKNVYLVVSS---S 89

Db 363 QIVGVYGVNTPVPS---SVPLKLVKQKVALENSFAPFSFKNVYLVVSS---S 89

Qy 90 LITVATLSDDEET---EMSNPTDMKFFLYLVLESPLF---CAUTSSLEVQCHI 144

Db 433 VILGQVADISFPCWCSDDSLTSYK---IQVDESPFDMFATVQCEVLTCHP 480

Qy 145 P-RHNSHRLGMLSNICDPECKCKNSTIYFNENBQKLOCTQLNPLNLTSLIT 203

Db 491 KPTFSSER---YV-----CNDKHC-----ELPLAL--SSGLVCKNNLVLT 522

Qy 204 T-----CIFSSGSHRVALPIPL 233

Db 533 LILGVSSEDGNGWQNGDGEFEFVAVL 536

RESULT 11

Sequence 6, Application US/09818247

Patent No. US200102657A1

GENERAL INFORMATION NUMBER C.

APPLICANT: Moskov, Keith E.

APPLICANT: Chaplin, Steven J.

TITLE OF INVENTION: Ligands directed to the No. US20020102657A1-Secretory Component

ANTIBODIES TO PLANT PROTECTION PROTEINS IN PLANTS AND THEIR USE

FILE REFERENCE: 18062E-0091005

CURRENT APPLICATION NUMBER: US/09/818,247

PRIOR FILING DATE: 2001-01-26

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-03-27

SOFTWARE: Patent Ver. 2.1

SEQ ID NO: 6

TYPE: PRT

ORGANISM: Oryctolagus cuniculus

OTHER INFORMATION: rabbit polyclonal immunoglobulin receptor (p98)

US-09-818-247-6

Query Match

Best Local Similarity 22.04; Pred. No. 0.11;

Matches 47; Conservative 39; Mismatches 79; Indels 49; Gaps

39 GNVTWP-----SVPLKLVKQKVALENSFAPFSFKNVYLVVSS---S 89

Db 363 QIVGVYGVNTPVPS---SVPLKLVKQKVALENSFAPFSFKNVYLVVSS---S 89

Qy 90 LITVATLSDDEET---EMSNPTDMKFFLYLVLESPLF---CAUTSSLEVQCHI 144

Db 433 VILGQVADISFPCWCSDDSLTSYK---IQVDESPFDMFATVQCEVLTCHP 480

Qy 145 P-RHNSHRLGMLSNICDPECKCKNSTIYFNENBQKLOCTQLNPLNLTSLIT 203



1 PRIOR FILING DATE: 1998-06-04  
 2 PRIOR APPLICATION NUMBER: 60/098028  
 3 PRIOR FILING DATE: 1998-06-04  
 4 PRIOR APPLICATION NUMBER: 60/098029  
 5 PRIOR FILING DATE: 1998-06-04  
 6 PRIOR APPLICATION NUMBER: 60/098030  
 7 PRIOR FILING DATE: 1998-06-04  
 8 PRIOR APPLICATION NUMBER: 60/098033  
 9 PRIOR FILING DATE: 1998-06-04  
 10 PRIOR APPLICATION NUMBER: 60/098036  
 11 PRIOR FILING DATE: 1998-06-04  
 12 PRIOR APPLICATION NUMBER: 60/098167  
 13 PRIOR FILING DATE: 1998-06-04  
 14 PRIOR APPLICATION NUMBER: 60/098202  
 15 PRIOR FILING DATE: 1998-06-05  
 16 PRIOR APPLICATION NUMBER: 60/098212  
 17 PRIOR FILING DATE: 1998-06-05  
 18 PRIOR APPLICATION NUMBER: 60/098217  
 19 PRIOR FILING DATE: 1998-06-05  
 20 PRIOR APPLICATION NUMBER: 60/098655  
 21 PRIOR FILING DATE: 1998-06-10  
 22 PRIOR APPLICATION NUMBER: 60/098734  
 23 PRIOR FILING DATE: 1998-06-10  
 24 PRIOR APPLICATION NUMBER: 60/098738  
 25 PRIOR FILING DATE: 1998-06-10  
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 27 PRIOR FILING DATE: 1998-06-10  
 28 PRIOR APPLICATION NUMBER: 60/098810  
 29 PRIOR FILING DATE: 1998-06-10  
 30 PRIOR APPLICATION NUMBER: 60/098824  
 31 PRIOR FILING DATE: 1998-06-10  
 32 PRIOR APPLICATION NUMBER: 60/098826  
 33 PRIOR FILING DATE: 1998-06-10  
 34 PRIOR APPLICATION NUMBER: 60/098858  
 35 PRIOR FILING DATE: 1998-06-11  
 36 PRIOR APPLICATION NUMBER: 60/098861  
 37 PRIOR FILING DATE: 1998-06-11  
 38 PRIOR APPLICATION NUMBER: 60/098876  
 39 PRIOR FILING DATE: 1998-06-11  
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 43 PRIOR FILING DATE: 1998-06-16  
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 59 PRIOR FILING DATE: 1998-06-17  
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 61 PRIOR FILING DATE: 1998-06-16  
 62 PRIOR APPLICATION NUMBER: 60/099907  
 63 PRIOR FILING DATE: 1998-06-16  
 64 PRIOR APPLICATION NUMBER: 60/099947  
 65 PRIOR FILING DATE: 1998-06-19  
 66 PRIOR APPLICATION NUMBER: 60/099948  
 67 PRIOR FILING DATE: 1998-06-19  
 68 PRIOR APPLICATION NUMBER: 60/099952  
 69 PRIOR FILING DATE: 1998-06-22  
 70 PRIOR APPLICATION NUMBER: 60/099246  
 71 PRIOR FILING DATE: 1998-06-22

1 PRIOR APPLICATION NUMBER: 60/090352  
 2 PRIOR FILING DATE: 1998-06-22  
 3 PRIOR APPLICATION NUMBER: 60/090254  
 4 PRIOR FILING DATE: 1998-06-23  
 5 PRIOR APPLICATION NUMBER: 60/090349  
 6 PRIOR FILING DATE: 1998-06-23  
 7 PRIOR APPLICATION NUMBER: 60/090355  
 8 PRIOR FILING DATE: 1998-06-23  
 9 PRIOR APPLICATION NUMBER: 60/090429  
 10 PRIOR FILING DATE: 1998-06-24  
 11 PRIOR APPLICATION NUMBER: 60/090431  
 12 PRIOR FILING DATE: 1998-06-24  
 13 PRIOR APPLICATION NUMBER: 60/090435  
 14 PRIOR FILING DATE: 1998-06-24  
 15 PRIOR APPLICATION NUMBER: 60/090444  
 16 PRIOR FILING DATE: 1998-06-24  
 17 PRIOR APPLICATION NUMBER: 60/090445  
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 19 PRIOR APPLICATION NUMBER: 60/090472  
 20 PRIOR FILING DATE: 1998-06-24  
 21 PRIOR APPLICATION NUMBER: 60/090535  
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 26 PRIOR FILING DATE: 1998-06-24  
 27 PRIOR APPLICATION NUMBER: 60/090557  
 28 PRIOR FILING DATE: 1998-06-24  
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 30 PRIOR FILING DATE: 1998-06-25  
 31 PRIOR APPLICATION NUMBER: 60/090678  
 32 PRIOR FILING DATE: 1998-06-25  
 33 PRIOR APPLICATION NUMBER: 60/090690  
 34 PRIOR FILING DATE: 1998-06-25  
 35 PRIOR APPLICATION NUMBER: 60/090694  
 36 PRIOR FILING DATE: 1998-06-25  
 37 PRIOR APPLICATION NUMBER: 60/090695  
 38 PRIOR FILING DATE: 1998-06-25  
 39 PRIOR APPLICATION NUMBER: 60/090696  
 40 PRIOR FILING DATE: 1998-06-25  
 41 PRIOR APPLICATION NUMBER: 60/090862  
 42 PRIOR FILING DATE: 1998-06-26  
 43 PRIOR APPLICATION NUMBER: 60/090863  
 44 PRIOR FILING DATE: 1998-06-26  
 45 PRIOR APPLICATION NUMBER: 60/091160  
 46 PRIOR FILING DATE: 1998-07-01  
 47 PRIOR APPLICATION NUMBER: 60/091478  
 48 PRIOR FILING DATE: 1998-07-02  
 49 PRIOR APPLICATION NUMBER: 60/091544  
 50 PRIOR FILING DATE: 1998-07-01  
 51 PRIOR APPLICATION NUMBER: 60/091519  
 52 PRIOR FILING DATE: 1998-07-02  
 53 PRIOR APPLICATION NUMBER: 60/091626  
 54 PRIOR FILING DATE: 1998-07-02  
 55 PRIOR APPLICATION NUMBER: 60/091633  
 56 PRIOR FILING DATE: 1998-07-02  
 57 PRIOR APPLICATION NUMBER: 60/091978  
 58 PRIOR FILING DATE: 1998-07-07  
 59 PRIOR APPLICATION NUMBER: 60/091982  
 60 PRIOR FILING DATE: 1998-07-07  
 61 PRIOR APPLICATION NUMBER: 60/092182  
 62 PRIOR FILING DATE: 1998-07-09

Query Match 6 98; Score 90; DB 9; Length 335;

Best Local Similarity 21.78; Prod. No. 0 91;

Matches 95; Conservativeness 42; Mismatches 107; Indels 42; Gaps 13;

OY 31 00TGVVYGVYVFWVW-PLKXVJMKKONKVALE-NSFWFASXKNVLTQVSG 88

DB 27 KEIIGVGAGVATPLAKXKVVDSVFWTFVLTQVGGTITLVQNNKMRVDFQSG 86

OY 89 --SITVMTSSDEEY-----ENESFWITDVFVLTLSLPTLICAL--TNG 136





Do 254 ROBE 257

Search completed: January 28, 2003, 08:53:00  
Job time : 83.077 secs



XX 12-MAR-1991: 91US-065791.  
 PR 07-OCT-1991: 91US-0770967.  
 PA (BIO) (BIOGEN INC.)  
 XX Miller GT, Rosa MD, Wallner BP.  
 DR N-PS08: A028684.  
 DR N-PS08: 1992-309760/28.  
 DR CD2-binding domain of lymphocyte function associated antigen-3  
 PT and DNA - for diagnosing and treating inflammation and  
 PT autoimmune diseases, e.g. systemic lupus erythematosus and  
 PT rheumatoid arthritis  
 XX CHAIN 13: Fig 12: 89pp: English.  
 CC The plasmid pSAB152 contains the DNA sequence encoding the LFA-3  
 CC signal sequence, the amino terminal 92 amino acids of mature LFA-3,  
 CC constant domains of IgG1 (see A028679.9 and A028681.2 for details of  
 CC the construction of pSAB152). A NotI fragment containing the coding  
 CC sequence of pSAB152 was used in the construction of expression  
 CC vectors pMDR102152 which were used to transform E. coli to  
 CC achieve continuous expression of LFA3/3P. The fusion protein can  
 CC bind to CD2 and inhibit T cell activation, making it useful to  
 CC inhibit autoimmune inflammation, autoimmune disease and  
 CC immunomodulation.  
 XX Sequence 347 AA;  
 Query Match 100.00: Score 1856; DB 13: Length 347;  
 Best Local Similarity 100.00: Pred. No. 2,1e-128;  
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 WVGSDAGRALGVSVCLLKGFGICFCSQITGYGVNTFVNSPFLVIAKKK 60  
 Db 1 WVGSDAGRALGVSVCLLKGFGICFCSQITGYGVNTFVNSPFLVIAKKK 60  
 Oy 61 DVALENSAFKSNFYLDVYSGSLTMTLSDEDEYDMSNPITDMKFELV 120  
 Db 61 DVALENSAFKSNFYLDVYSGSLTMTLSDEDEYDMSNPITDMKFELV 120  
 Oy 121 DKTHCPCPAPELGGSVFLPPKPTLMSRTPTVYGVVNSDEPVENYVD 180  
 Db 121 DKTHCPCPAPELGGSVFLPPKPTLMSRTPTVYGVVNSDEPVENYVD 180  
 Oy 181 GVEVNNATKFPEDYVSTVRSVLYLHQDMJGKEYCKVSNKALPAPEKTSK 240  
 Db 181 GVEVNNATKFPEDYVSTVRSVLYLHQDMJGKEYCKVSNKALPAPEKTSK 240  
 Oy 191 GVEVNNATKFPEDYVSTVRSVLYLHQDMJGKEYCKVSNKALPAPEKTSK 240  
 Db 191 GVEVNNATKFPEDYVSTVRSVLYLHQDMJGKEYCKVSNKALPAPEKTSK 240  
 Oy 241 QDRPEQVYVLPSSRDILTKNVSCLTVKGFYSVDIAVMSNQPKNNKTPVLGS 300  
 Db 241 QDRPEQVYVLPSSRDILTKNVSCLTVKGFYSVDIAVMSNQPKNNKTPVLGS 300  
 Oy 301 DGSFPLVLSKTVSRMQQVNTSCSMHIALNNHTQISLSLPCK 347  
 Db 301 DGSFPLVLSKTVSRMQQVNTSCSMHIALNNHTQISLSLPCK 347  
 RESULT 2  
 AA#83136  
 AC AA#83136 standard; Protein. 347 AA.  
 XX AA#83136;  
 XX 24-JUL-2000 (first entry)  
 XX Human transmembrane LFA-3/3G fusion protein LFA3/3P.  
 DE LFA3; CD2; cell signalling; modulation; lymphocyte; T cell;  
 KM memory effector T lymphocyte; psoriatic arthritis;

KW rheumatoid arthritis, multiple sclerosis, atopic dermatitis;  
 KW psoriasis, inflammatory bowel disease, Crohn's disease,  
 KW ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;  
 KW therapy.  
 OS Homo sapiens.  
 XX W030001313-42.  
 XX 09-MAR-2000.  
 PF 31-AUG-1999: 99MO-US20026.  
 XX 31-AUG-1998: 98US-0098456.  
 PA (BIO) (BIOGEN INC.)  
 XX Masjlavy D;  
 DR WPI: 2000-282928/24.  
 DR N-PS08: A029401.  
 PF Selective modulation of memory effector T lymphocytes by administration  
 PF of a CD2 binding agent which inhibits the CD2/LFA-3 interaction useful  
 PF in various conditions such as inflammatory bowel diseases, psoriatic  
 PF arthritis  
 XX Disclosure: Page 75-76; 76pp: English.  
 CC Modulation of LFA3/CD2 interaction by administration of a CD2 binding  
 CC agent, which inhibits the CD2/LFA-3 interaction and thus modulates the  
 CC memory effector T lymphocytes. The method can be used for treating a  
 CC condition in a subject where the condition is characterized by memory  
 CC effector T lymphocytes. The method also includes the use of the  
 CC condition such as psoriatic arthritis, rheumatoid arthritis,  
 CC multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel  
 CC diseases, Crohn's disease, ulcerative colitis, Crohn's disease, Crohn's  
 CC lymphoma and where the method comprises administering to the subject  
 CC an amount of CD2 binding agent sufficient to modulate the memory  
 CC effector T lymphocytes. The method also includes the use of the  
 CC specific interactions for all antigens present. Inhibition of T cell  
 CC activation, no general immunosuppression, and possibly induction of  
 CC tolerance.  
 XX Sequence 347 AA;  
 Query Match 100.00: Score 1856; DB 21: Length 347;  
 Best Local Similarity 100.00: Pred. No. 2,1e-128;  
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 WVGSDAGRALGVSVCLLKGFGICFCSQITGYGVNTFVNSPFLVIAKKK 60  
 Db 1 WVGSDAGRALGVSVCLLKGFGICFCSQITGYGVNTFVNSPFLVIAKKK 60  
 Oy 61 DVALENSAFKSNFYLDVYSGSLTMTLSDEDEYDMSNPITDMKFELV 120  
 Db 61 DVALENSAFKSNFYLDVYSGSLTMTLSDEDEYDMSNPITDMKFELV 120  
 Oy 121 DKTHCPCPAPELGGSVFLPPKPTLMSRTPTVYGVVNSDEPVENYVD 180  
 Db 121 DKTHCPCPAPELGGSVFLPPKPTLMSRTPTVYGVVNSDEPVENYVD 180  
 Oy 181 GVEVNNATKFPEDYVSTVRSVLYLHQDMJGKEYCKVSNKALPAPEKTSK 240  
 Db 181 GVEVNNATKFPEDYVSTVRSVLYLHQDMJGKEYCKVSNKALPAPEKTSK 240  
 Oy 241 QDRPEQVYVLPSSRDILTKNVSCLTVKGFYSVDIAVMSNQPKNNKTPVLGS 300  
 Db 241 QDRPEQVYVLPSSRDILTKNVSCLTVKGFYSVDIAVMSNQPKNNKTPVLGS 300  
 Oy 301 DGSFPLVLSKTVSRMQQVNTSCSMHIALNNHTQISLSLPCK 347  
 Db 301 DGSFPLVLSKTVSRMQQVNTSCSMHIALNNHTQISLSLPCK 347







PA (RBE\*) REGENERON PHARM INC.  
 XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
 XX WPI: 2001-071076/08.  
 XX R-780B: AA931076.  
 DR Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
 PT and its fragments, useful for diagnosis, evaluation, and treatment of  
 PT diseases associated with the gene expression and for producing model  
 PT systems.  
 XX Claim 49; Fig 24; 15pp; English.  
 CC This sequence represents a fusion protein of the invention between  
 CC the Fli1 receptor and the PC region of IgC. The specification relates  
 CC to modified chemical polypeptides are preferably Fli1 receptor polypeptides  
 CC that have been modified to improve their pharmacokinetic profile. The  
 CC polypeptides can be used to increase or inhibit plasma leakage and/or  
 CC vascular permeability in a mammal.  
 XX Sequence 458 AA:  
 50 Query Match 68.2%; Score 1265; DB 22; Length 458;  
 Best Local Similarity 78.7%; Pred. No. 7.7e-85;  
 Matches 248; Conservative 15; Mismatches 40; Indels 12; Gaps 4;  
 OY 40 NTTFVPSNPFLAEVLR-KQKDAVLENSERAFSEKFNKVIYDTYSSLIYNLIS 97  
 DB 149 NTFATFELNGI-DMNRYFSSKHQKLVNGLDTQSSSEMKFELST---LTIQVTR 203  
 OY 98 SDDIEEMSPNITDPMFLV-----DKTHCPQCPAPELGGSVFLPPKPTLM 152  
 DB 204 SDQGLTCAASSGLMTKNSFTVVRKQPKDHTCPAPELGGSVFLPPKPTLM 263  
 OY 153 TSPTSPCTCVYVSHSDPQKFNWYGVCHVYHAKTPEKQVNSTYKVSVLTVL 212  
 DB 264 TSRTPEVTCVYVSHSDPQKFNWYGVCHVYHAKTPEKQVNSTYKVSVLTVL 323  
 OY 213 MNGKCKYKCNKALPAETKTSKAGQKQPREQVYLPSPDRSLTKNQSLCLVGF 272  
 DB 324 MNGKCKYKCNKALPAETKTSKAGQKQPREQVYLPSPDRSLTKNQSLCLVGF 383  
 OY 273 YFSIDAVNMSQKQPNKNTTPPVLDSSGFFYSKLVTKSMQKQNVFSCVMBAL 332  
 DB 384 YFSIDAVNMSQKQPNKNTTPPVLDSSGFFYSKLVTKSMQKQNVFSCVMBAL 443  
 OY 333 NNITVTKQSLSPCK 347  
 DB 444 NNITVTKQSLSPCK 458  
 RESULT 7  
 AA975594  
 ID AA975594 standard; Protein: 458 AA.  
 AC AA975594;  
 XX 05-APR-2001 (first entry)  
 DE Fli1 receptor fusion protein Fli1D3.FcetaCl(a).  
 XX Fli1 receptor; fusion protein; chemotic protein; pharmacokinetic;  
 KW plasma leakage; vascular permeability; IgG Fc region.  
 XX Unidentified.  
 XX MO200075319-AL.  
 PM 14-DEC-2000.  
 XX 23-MAY-2000; 2000MO-DS1142.

XX 08-JUN-1999; 99US-0138133.  
 PA (RBE\*) REGENERON PHARM INC.  
 XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
 XX WPI: 2001-071076/08.  
 XX R-780B: AA931076.  
 DR Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
 PT and its fragments, useful for diagnosis, evaluation, and treatment of  
 PT diseases associated with the gene expression and for producing model  
 PT systems.  
 XX Claim 49; Fig 21; 15pp; English.  
 CC This sequence represents a fusion protein of the invention between  
 CC the Fli1 receptor and the PC region of IgC. The specification relates  
 CC to modified chemical polypeptides are preferably Fli1 receptor polypeptides  
 CC that have been modified to improve their pharmacokinetic profile. The  
 CC polypeptides can be used to increase or inhibit plasma leakage and/or  
 CC vascular permeability in a mammal.  
 XX Sequence 458 AA:  
 50 Query Match 68.1%; Score 1263.5; DB 22; Length 458;  
 Best Local Similarity 78.0%; Pred. No. 9.9e-85;  
 Matches 248; Conservative 15; Mismatches 40; Indels 15; Gaps 4;  
 OY 40 NTTFVPSNPFLAEVLR-KQKDAVLENSERAFSEKFNKVIYDTYSSLIYNLIS 97  
 DB 149 NTFATFELNGI-DMNRYFSSKHQKLVNGLDTQSSSEMKFELST---LTIQVTR 200  
 OY 98 SDDIEEMSPNITDPMFLV-----DKTHCPQCPAPELGGSVFLPPKPTLM 149  
 DB 201 SDQGLTCAASSGLMTKNSFTVVRKQPKDHTCPAPELGGSVFLPPKPTLM 260  
 OY 150 TSPTSPCTCVYVSHSDPQKFNWYGVCHVYHAKTPEKQVNSTYKVSVLTVL 209  
 DB 261 TSRTPEVTCVYVSHSDPQKFNWYGVCHVYHAKTPEKQVNSTYKVSVLTVL 320  
 OY 210 MNGKCKYKCNKALPAETKTSKAGQKQPREQVYLPSPDRSLTKNQSLCLV 269  
 DB 320 MNGKCKYKCNKALPAETKTSKAGQKQPREQVYLPSPDRSLTKNQSLCLV 380  
 OY 272 YFSIDAVNMSQKQPNKNTTPPVLDSSGFFYSKLVTKSMQKQNVFSCVMBH 329  
 DB 381 YFSIDAVNMSQKQPNKNTTPPVLDSSGFFYSKLVTKSMQKQNVFSCVMBH 440  
 OY 330 NNITVTKQSLSPCK 347  
 DB 441 NNITVTKQSLSPCK 458  
 RESULT 8  
 AA954408  
 ID AA954408 standard; Protein: 744 AA.  
 AC AA954408;  
 XX 11-SEP-2000 (first entry)  
 DE Human VCM-1/IgG1-FC fusion protein.  
 XX Human; cellular adhesion molecule; ACM; neopteric; antiapoptotic;  
 KW neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;  
 KW dementia; epilepsy; schizophrenia; peripheral nerve injury;  
 XX diabetic neuropathy; fusion protein.  
 XX Homo sapiens.

PK W02000032633-A1.  
 XX 08-JUN-2000.  
 PP 02-DEC-1999; 99NO-US28878.  
 XX 02-DEC-1999; 98US-0203462.  
 XX (100%) ICOS CORP.  
 PA booktra DM, Loughney K, Stauton DE, Vasquez R;  
 XX WPI: 2000-422952/36.  
 DR N-YSDB: AAH30422.  
 XX  
 XX Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful  
 XX for diagnosing, preventing and treating diseases associated with ACAM  
 XX expression and activity, e.g., epilepsy and schizophrenia.  
 XX Example 5: page 174-176; 187pp; English.  
 XX  
 CC The present sequence is a fusion protein comprising part of human  
 CC VCAM-1 and the Fc region of human IgG1. The sequence encoding this  
 CC fusion protein is designated pBR24/195, which encodes the hinge and constant  
 CC CIP-CH3 domains of human IgG1. The sequence was then ligated into  
 CC the fusion vector pBR24 and transformed into *Escherichia coli* cells  
 CC using the fusion vector pBR24 and transformed into *Escherichia coli* cells  
 CC involving ACAM4/195-Fc and ACAM4/195-Fc fusion proteins. ACAM4 and  
 CC ACAM6 are human fetal brain cDNA clones containing alternatively  
 CC spliced exons. ACAM4 and ACAM6 are nucleic acid sequences encoding  
 CC ACAM. ACAM nucleic acids and polypeptides may be used in the prevention,  
 CC treatment and diagnosis of diseases associated with inappropriate ACAM  
 CC expression. ACAM nucleic acids and polypeptides may also be used to  
 CC rectify mutations or deletions in a patient's genome that affect the  
 CC expression of ACAM or to supplement deficient ACAM production in a  
 CC patient's genome. ACAM nucleic acids and polypeptides may be used to  
 CC administered to down-regulate ACAM expression. The nucleotide sequence  
 CC may also be used as a DNA probe in diagnostic assays (e.g., PCR) to  
 CC detect the presence of ACAM in a sample. The amino acid sequences in  
 CC samples, and hence determine which patients may be in need of  
 CC restorative therapy. ACAM polypeptides may be used as antigens in the  
 CC development of vaccines for the prevention of diseases associated with  
 CC ACAM expression and activity.  
 XX  
 XX Sequence 744 AA;  
 XX  
 XX Query Match Best Local Similarity 75.3%; Pred. No. 2, 2e-84;  
 XX Matches 251; Conservations 15; Mismatches 40; Indels 28; Gaps 6;  
 OY 35 GYTYNQ--VTFVNSVPLKLVKQKRVKVALENSFSAFSSFN-----RVILD 84  
 DB 414 GLNNSYTSVSVSVPLDLRIEILKGLT-LNLTLEDTDWSLENSLSEWPT 472  
 OY 85 TVSG--SEITVWLSDESDYDSESHITDPMKFFVY-----DTHFCPCPA 131  
 DB 473 FIEDRGALVCAKRLHOMEPFGQISTGTVVWVAPDFKSKITFCPCPA 528  
 OY 132 FIEDRGALVCAKRLHOMEPFGQISTGTVVWVAPDFKSKITFCPCPA 528  
 DB 473 FIEDRGALVCAKRLHOMEPFGQISTGTVVWVAPDFKSKITFCPCPA 528  
 OY 132 FIEDRGALVCAKRLHOMEPFGQISTGTVVWVAPDFKSKITFCPCPA 528  
 DB 473 FIEDRGALVCAKRLHOMEPFGQISTGTVVWVAPDFKSKITFCPCPA 528  
 OY 192 REDQNSTVSHVTVLHMDLNKCTCKVSKALPAIDRTLSAKGQDFPQVLT 251  
 DB 589 REDQNSTVSHVTVLHMDLNKCTCKVSKALPAIDRTLSAKGQDFPQVLT 251  
 OY 252 PFQSRGLKQVSLKCVLQFSDQIVAVESNSDFPNKNTVPLVDSGDSFSLKLT 311  
 DB 649 PFQSRGLKQVSLKCVLQFSDQIVAVESNSDFPNKNTVPLVDSGDSFSLKLT 311  
 OY 312 VQKSRQSQGVFSCVMEALINIVITKSLISGPK 347  
 DB 705 VQKSRQSQGVFSCVMEALINIVITKSLISGPK 744

DB 705 VQKSRQSQGVFSCVMEALINIVITKSLISGPK 744  
 PSBLU2 9  
 AY84565  
 XX ID ANY84565 standard: Protein: 633 AA.  
 AC AY84565;  
 XX 21-AUG-2000 (first entry)  
 XX Amino acid sequence of a CD-20 specific chimeric receptor.  
 DE CD-20 specific receptor; CD-20 specific redirected T cell; leukemia;  
 CC CD20+ malignancy; non-Hodgkin's lymphoma; myoblastic chemotherapy;  
 KW stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis.  
 CC  
 OS Synthetic.  
 OS Msa sp.  
 PH Key Location/Qualifiers  
 FT Peptide 27..86 /note= "signal peptide from murine 766.66 antibody  
 FT Region 21..126 /note= "alpha 1 hinge chain"  
 FT Peptide /note= "anti-CD20 variable regions"  
 FT Region 283..392 /note= "CS18 linker"  
 FT Region 393..489 /note= "alpha 2 hinge region"  
 FT Region 500..522 /note= "CH3 region"  
 FT Region 522..633 /note= "CD4 transmembrane region"  
 FT Region 522..633 /note= "zeta chain"  
 PN W02000032573-A2.  
 XX 27-APR-2000.  
 XX WPI: 2000-730476/29.  
 XX 20-OCT-1999; 99NO-US24484.  
 XX 20-OCT-1998; 98US-0105014.  
 XX  
 XX (CITY) CITY OF HOPE.  
 XX Raubitschek A, Jensen MC, Wu AM;  
 XX WPI: 2000-730476/29.  
 XX N-PSDB: AA15019.  
 XX  
 XX Genetically engineered CD20-specific redirected T cells useful for  
 XX treatment of CD20+ malignancies, such as lymphoma or CD20+  
 XX acute or chronic leukemia, and autoimmune disease.  
 XX Claim 10: page 53-55; 58pp; English.  
 XX The present sequence represents a synthetic CD20-specific chimeric  
 XX receptor comprising an intracellular signalling domain, a transmembrane  
 XX domain, and an extracellular domain. The extracellular domain comprising  
 XX a CD20-specific recognition domain. The intracellular domain comprising  
 XX a redirected T cells are useful for treating a CD20+ malignancy, such  
 XX as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a  
 XX stem cell rescue. The genetically engineered CD20-specific redirected  
 XX T cells are also useful for abrogating an untoward T cell function, such  
 XX as autoimmune disease (lupus or rheumatoid arthritis) in a patient.  
 XX Sequence 633 AA;

Query Match 67.6% Score 125.5; DB 21: Length 633;  
 Best Local Similarity 72.5%; Prod. No. 5.6e-04;  
 Matches 241; Conservative 5; Mismatches 25; Indels 21; Gaps 2;

Oy 77 FKNVLTDTYSSTT-----MUTSODEETSMSPNITDMKFLV-----120  
 Db 208 FKNVLTDTYSSTT-----MUTSODEETSMSPNITDMKFLV-----120  
 Oy 121 -----RPRGQPCAPNELGCGSVFLPKPOTLAIERTLVSQVWVSDRQV 175  
 Db 268 RPRGQPCAPNELGCGSVFLPKPOTLAIERTLVSQVWVSDRQV 175  
 Oy 268 DRSSQDHTCFPCFAPNELGCGSVFLPKPOTLAIERTLVSQVWVSDRQV 327  
 Db 176 DRSSQDHTCFPCFAPNELGCGSVFLPKPOTLAIERTLVSQVWVSDRQV 327  
 Oy 378 MRYVDQVYVNAKTFPRERQDHTCFPCFAPNELGCGSVFLPKPOTLAIERT 387  
 Db 378 MRYVDQVYVNAKTFPRERQDHTCFPCFAPNELGCGSVFLPKPOTLAIERT 387  
 Oy 213 ISANQGPQRPOTVLPSPRDELITNVSILCLVKGTFVDAVENSQGPENNTKP 295  
 Db 213 ISANQGPQRPOTVLPSPRDELITNVSILCLVKGTFVDAVENSQGPENNTKP 295  
 Oy 386 ISANQGPQRPOTVLPSPRDELITNVSILCLVKGTFVDAVENSQGPENNTKP 447  
 Db 386 ISANQGPQRPOTVLPSPRDELITNVSILCLVKGTFVDAVENSQGPENNTKP 447  
 Oy 296 PYLSDGSGFYSKVLTVKSRQGGQFVSVMHIALHNTTOKSLSLSPCK 347  
 Db 448 PYLSDGSGFYSKVLTVKSRQGGQFVSVMHIALHNTTOKSLSLSPCK 347  
 Db 448 PYLSDGSGFYSKVLTVKSRQGGQFVSVMHIALHNTTOKSLSLSPCK 347

RESULT 10  
 ID AM950207 standard; Protein: 477 AA.  
 XX 10-MAY-1999 (first entry)  
 XX AM950207;  
 DE hB7.2Fc soluble fusion protein.  
 XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;  
 XX CD86; T cell activation; inhibitor; graft versus host disease;  
 XX transplant rejection; allograft rejection; autoimmune disease;  
 XX allergy; therapy; human; antibody; hB7.1fc.  
 OS Chimeric \* Homo sapiens.  
 OS Chimeric - synthetic.

Key Location/Qualifiers  
 PE Peptide 1..16 \*potential eukaryotic secretory signal  
 FT Note= "human hB7.2 domain"  
 FT Domain 17..239  
 FT Note= "human hB7.2 (mature protein) extracellular  
 FT Peptide 240..245 domain"  
 FT Note= "introduced by PCR cloning strategy"  
 FT Protein Note= "human IgG1-Fc (hinge-CH2-CH3)"  
 XX X09858945-A2.  
 PD 30-DEC-1998.  
 XX 22-JUN-1998; 98NO-E903791.  
 XX 20-JUN-1997; 97EP-0870592.  
 PA (LNK)- INNOGENETICS NV.  
 PA Bosman A, Blyse M, Lorre K, Sblon E;  
 DR WFI: 1995-105615/09.  
 XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
 PT immune diseases including allograft rejection

PS Example 3.1.1.3; Fig 3; 182pp; English.  
 XX This 54 kDa soluble fusion protein, termed hB7.2Fc, is composed of  
 CC hB7.2 extracellular domain fused  
 CC C-terminally to human IgG1-Fc. It was produced by PCR  
 CC amplification of hB7.2 cDNA in plasmid pGEMTneohB7.2, and  
 CC in pVaxB7.2-Fc (2003004) baculovirus transfer plasmid. The invention  
 CC relates to molecules such as antibodies, trivalent and tetravalent  
 CC or cross-react with B7.1 and B7.2 expressed on professional  
 CC antigen presenting cells leading to the inhibition of  
 CC antigen specific T cell activation. Methods to produce such  
 CC diseases of the immune system, in particular graft rejection, graft  
 CC versus host disease, allergy and autoimmune diseases (claimed).

Query Match 67.6% Score 125.5; DB 20: Length 477;  
 Best Local Similarity 78.3%; Prod. No. 4.4e-84;  
 Matches 241; Conservative 15; Mismatches 26; Indels 26; Gaps 4;

Oy 55 LMKQGVDAVENSQFPRASQKPNVLYTQVSYVNLVSQDQ-----EYDME- 106  
 Db 179 LMKQGVDAVENSQFPRASQKPNVLYTQVSYVNLVSQDQ-----EYDME- 106  
 Oy 107 -----SPNITDMKFLVYKTKPCPCAPNELGCGSVFLPKPOTLAIERTPE 158  
 Db 233 PQQPQDSKGLQKESK-----CKTHFCPCFAPNELGCGSVFLPKPOTLAIERTPE 208  
 Oy 159 VTCVYVSDVSHEDPEFVKNVGVGVNAKTFPRERQDHTCFPCFAPNELGCGSV 218  
 Db 289 VTCVYVSDVSHEDPEFVKNVGVGVNAKTFPRERQDHTCFPCFAPNELGCGSV 348  
 Oy 219 YCKYKYNALPATERTISKANQGPQRPOTVLPSPRDELITNVSILCLVKGTFVSDIA 278  
 Db 349 YCKYKYNALPATERTISKANQGPQRPOTVLPSPRDELITNVSILCLVKGTFVSDIA 408  
 Oy 279 YKSGVSGQPNKTFPRERQDHTCFPCFAPNELGCGSVFLPKPOTLAIERTHNTTOK 338  
 Db 409 YKSGVSGQPNKTFPRERQDHTCFPCFAPNELGCGSVFLPKPOTLAIERTHNTTOK 468  
 Oy 339 KSLSLSLSPCK 347  
 Db 469 KSLSLSLSPCK 477

RESULT 11  
 AM973514 standard; Protein: 388 AA.  
 XX AM973514;  
 XX 02-MAR-1999 (first entry)  
 XX 02-MAR-1999 (first entry)  
 XX Human TGF-betaII:Fc protein sequence.  
 XX Transforming growth factor-beta receptor; TGF-beta receptor; arthritis;  
 XX fusion protein; fibroproliferative disorder; diabetic nephropathy;  
 XX collagen vascular disorder; therapy; human.  
 XX Homo sapiens.  
 XX X09848024-A1.  
 PM 29-OCT-1998.  
 XX 16-APR-1998; 98NO-US07597.  
 XX 18-APR-1997; 97US-0044641.





Best Local Similarity	90.7%	Prod. No. 7.3e-84;	4; Mismatches	3; Indels	17; Gaps
QY	97	S30E-----DVEYEMSPNITDQKFLVYDHTCTPCFAPPELGGPSVF	148		
Db	135	STDCNHLIFSEETYSFDL-----VDMTHCTPCFAPPELGGPSVF	169		
QY	149	DTLMSLPPPCVYDMSDEPKYKYNVGVCHVKNKATPEFVNSYRSTGQVRY	208		
Db	190	DTLMSLPPPCVYDMSDEPKYKYNVGVCHVKNKATPEFVNSYRSTGQVRY	249		
QY	190	DTLMSLPPPCVYDMSDEPKYKYNVGVCHVKNKATPEFVNSYRSTGQVRY	249		
QY	250	LQMDLAKKRYCKVSKMALPAPTKTISKAKGQPPQVYTPSPDEBLKKNVSLCL	268		
Db	250	LQMDLAKKRYCKVSKMALPAPTKTISKAKGQPPQVYTPSPDEBLKKNVSLCL	309		
QY	269	VAGTFPSDIAVMSNGSPENKWTTPYLDSDGSPFLSKLTVKSMQGNVFCRW	328		
Db	310	VAGTFPSDIAVMSNGSPENKWTTPYLDSDGSPFLSKLTVKSMQGNVFCRW	369		
QY	329	HEALNNHTYTKSLSPK 347			
Db	370	HEALNNHTYTKSLSPK 388			
RESUL 15					
AA971172					
10	AA971172	Standard: Protein: 497 AA.			
AC	AA971172:				
XX	04-DEC-2000	(first entry)			
XX	Human FGF-R1 Extracellular domain-Ig Fc fusion protein 3.				
DE	FGF-R: fibroblast growth factor receptor; extracellular domain: IgG1;				
XX	immunoglobulin; Q: oligomerization domain; FC region: fusion protein;				
KM	inhibitor dimer; anteposid; cytosolic; anti-diabetic; vulnary;				
XX	optimal biological; anti-proliferative.				
OS	Homo sapiens.				
PR					
Key	Location/Qualifiers				
FT	1..21				
FT	/label= FGF-R1_signal_peptide				
FT	2..267				
FT	/label= FGF-R1_extracellular_domain				
FT	516..517				
FT	/note= The Ig 1 segment and acid box are deleted*				
FT	/label= Ig_II_segment				
FT	157..222				
FT	/label= Linker				
FT	238..265				
FT	/label= Linker				
FT	/label= human_IgG1_Fc_region				
FT	/label= human_IgG1_Fc_region				
FT	/note= Contains hinge region and domains CH2 and CH3*				
XX	NO200046380-A2.				
XX	10-AUG-2000.				
PP	07-FEB-2000:	2000MD-US03166.			
XX	08-FEB-1999,	99US-0119002.			
XX	(CHIR ) CHIRON CORP.				
PA	Kavanaugh WM, Ballinger M;				
XX	WPI:4000-51495/46.				
DR	NF506, AA52157.				
XX	New polypeptide comprising a fibroblast growth factor receptor				

FT	extracellular domain fused to a heterologous oligomerization domain for				
XX	creating FGF-R, angiogenesis, or FGF receptor-mediated disorders				
XX	Claim 14: Page 58-59: 70up: Construct.				
XX	Novel fusion protein constructs comprise a fibroblast growth factor (FGF)				
CC	receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin				
CC	region, or a portion thereof, fused to a heterologous oligomerization				
CC	domain, or a portion thereof, in the hinge region, CH1, CH2, CH3 or CH4				
CC	region, or light chain of an immunoglobulin molecule, or a peptide with a				
CC	sequence capable of forming a stable complex with the FGF-R ECD, or a				
CC	peptide or basic FGF (bFGF) segment, is not necessary for binding of the				
CC	affinity for bFGF and heparin, protects the core of the molecule from				
CC	proteolysis, and abrogates the heparin requirement for bFGF binding. The				
CC	peptide, the FGF-R ECD fusion dimers are active as FGF antagonists at				
CC	subnanomolar concentrations and were 20-fold more potent than the FGF-R				
CC	antagonist, FGF-R ECD fusion dimers, in the treatment of tumor. The				
CC	fusion constructs are useful to treat FGF-angiogenesis, or				
CC	FGF-R-mediated disorders such as tumorogenesis (e.g. bladder, breast,				
CC	lung metastasis, and cervical tumors), neovascularization (e.g.				
CC	diabetic retinopathy), and hyper-proliferation of vascular smooth muscle cells (e.g.				
CC	scar) and postangioplasty and postatherectomy restenosis).				
CC	Sequence 497 AA:				
QY	Query Match	57.3%	Score 1249.5;	DB 21: Length 497;	
XX	Best Local Similarity	75.3%	Prod. No. 1.2e-83		
XX	Matches 247; Conservative	12; Mismatches 32; Indels	35; Gaps	5;	
QY	46	PSWPLKELV-----WKKNQVAVLSESTFASFSK---HNYLYTSGSLTYWL	95		
Db	183	FMPLPTVLTATGNTGDMVHLHJRWSEDAETCTCAGNSIGLSHSMULTY--L	240		
QY	96	TSSEDEDEMSPTDTPMFLVY-----DKFTCPCPAPELGGPSVF	141		
Db	241	DADEPAPNPSR-----LIGSSPGLQEPKSCNTHCTPCFAPPELGGPSVF	291		
QY	142	LFPPKPTALSRPPTCVYDMSDEPKYKYNVGVCHVKNKATPEFVNSYRSTGQVRY	201		
Db	292	LFPPKPTALSRPPTCVYDMSDEPKYKYNVGVCHVKNKATPEFVNSYRSTGQVRY	351		
QY	202	VYVYLVYDQMKKRYCKVSKMALPAPTKTISKAKGQPPQVYTPSPDEBLKKNVSLCL	261		
Db	352	VYVYLVYDQMKKRYCKVSKMALPAPTKTISKAKGQPPQVYTPSPDEBLKKNVSLCL	411		
QY	262	QNSCTCLCKVCFSDIAVMSNGSPENKWTTPYLDSDGSPFLSKLTVKSMQGNVFCRW	321		
Db	412	QNSCTCLCKVCFSDIAVMSNGSPENKWTTPYLDSDGSPFLSKLTVKSMQGNVFCRW	471		
QY	322	VPSYVMSHMLHNNHTYTKSLSPK 347			
Db	472	VPSYVMSHMLHNNHTYTKSLSPK 497			
QY	322	VPSYVMSHMLHNNHTYTKSLSPK 347			
Db	472	VPSYVMSHMLHNNHTYTKSLSPK 497			

Search completed: January 28, 2003, 08:42:02  
 Job time : 35.7806 secs





Db 181 GYVNNKATPREOYNTSTFVSVLVFLVLIQDLAKKCKVSNKALPAKTKTISAK 240  
 Qy 241 GQPREQVYVTLPSDEELKNOVSLCLVKCFITPSQIAVENMSQCFENKKTFFVDS 300  
 Db 241 GQPREQVYVTLPSDEELKNOVSLCLVKCFITPSQIAVENMSQCFENKKTFFVDS 300  
 Qy 301 DGSFPLSKLTVKDSRMOQGNVFCFSVMEHLAHNHTQKLSLSRCK 347  
 Db 301 DGSFPLSKLTVKDSRMOQGNVFCFSVMEHLAHNHTQKLSLSRCK 347

RESULT 2  
 US-09-796-033-8      Application US/09760033  
 Sequence 8      US/09760033  
 General Information:  
 APPLICANT: Masilav, Daniel  
 TITLE OF INVENTION: T-CELLS REGULATING MINOR EFFECTOR  
 CURRENT FILING DATE: 2001-07-27  
 FILE REFERENCE: 10274-044001 US/09/796, 033  
 PRIOR APPLICATION NUMBER: PCT/US99/20226  
 PRIOR FILING DATE: 1999-04-30  
 PRIOR FILING DATE: 1998-08-31  
 NUMBER OF SEQ ID NOS: 8  
 SEQ ID NO 8      HASKSQ for Windows Version 4.0

LENGTH: 347  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SIGNAL  
 DEFINITION: (48)  
 US-09-796-033-8

Query Match      100.0%; Score 1856; DB 10; Length 347;  
 Best Local Similarity      100.0%; Pred. No 1,7e-121;  
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAGSDAGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 60  
 Db 1 MYAGSDAGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 60  
 Qy 61 DVALENSGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 120  
 Db 61 DVALENSGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 120  
 Qy 61 DVALENSGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 120  
 Db 61 DVALENSGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 120  
 Qy 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Db 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Qy 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Db 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Qy 181 GYVNNKATPREOYNTSTFVSVLVFLVLIQDLAKKCKVSNKALPAKTKTISAK 240  
 Db 181 GYVNNKATPREOYNTSTFVSVLVFLVLIQDLAKKCKVSNKALPAKTKTISAK 240  
 Qy 241 GQPREQVYVTLPSDEELKNOVSLCLVKCFITPSQIAVENMSQCFENKKTFFVDS 300  
 Db 241 GQPREQVYVTLPSDEELKNOVSLCLVKCFITPSQIAVENMSQCFENKKTFFVDS 300  
 Qy 301 DGSFPLSKLTVKDSRMOQGNVFCFSVMEHLAHNHTQKLSLSRCK 347  
 Db 301 DGSFPLSKLTVKDSRMOQGNVFCFSVMEHLAHNHTQKLSLSRCK 347

RESULT 3  
 US-09-730-465-8      Application US/09730465  
 Sequence 6      US/09730465  
 Patent No: US20020094941  
 General Information:  
 APPLICANT: Cooper, Kevin D.

TITLE OF INVENTION: Method of Prophylaxis or Treatment of Action  
 Presenting Cell Driven Skin Conditions Using  
 Inhibitors of the CD2/LEA-3 Interaction  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: BOSTON  
 STATE: Massachusetts  
 COUNTRY: USA  
 COMPUTER FILE NAME:  
 COMPUTER FILE TYPE:  
 COMPUTER FILE SIZE:  
 COMPUTER FILE EXTENSION:  
 CURRENT APPLICATION DATA: US/09/730,465  
 FILING DATE: 05-Dec-2000  
 PRIOR APPLICATION DATA: PCT/US92/08755  
 FILING DATE: 05-Oct-1992  
 APPLICATION NUMBER: US 07/862,022  
 FILING DATE: 12-Apr-1992  
 APPLICATION NUMBER: US 07/770,969  
 FILING DATE: 07-Oct-1991

ATTORNEY/AGENT INFORMATION:  
 NAME/KEY: LAHIVE & COCKFIELD  
 REGISTRATION NUMBER: 35,965  
 REFERENCE/DOCKET NUMBER: BGP-111CP  
 TELECOMMUNICATIONS INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5841  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 TYPE: amino acid  
 LENGTH: 347 amino acids  
 MOLECULE TYPE: protein  
 US-09-730-465-8

Query Match      100.0%; Score 1856; DB 10; Length 347;  
 Best Local Similarity      100.0%; Pred. No 1,7e-121;  
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAGSDAGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 60  
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 Qy 61 DVALENSGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 120  
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 Db 61 DVALENSGALVSVCLLHRCFISQSOIQVGVYGVNTFVSNVPLKLVKKOR 120  
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 Db 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Qy 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Db 121 DNTHTCPQAPVLLGQGNFLFPKPKOTIAISFPEVTVGVSDPEKVMYD 180  
 Qy 181 GYVNNKATPREOYNTSTFVSVLVFLVLIQDLAKKCKVSNKALPAKTKTISAK 240  
 Db 181 GYVNNKATPREOYNTSTFVSVLVFLVLIQDLAKKCKVSNKALPAKTKTISAK 240  
 Qy 241 GQPREQVYVTLPSDEELKNOVSLCLVKCFITPSQIAVENMSQCFENKKTFFVDS 300  
 Db 241 GQPREQVYVTLPSDEELKNOVSLCLVKCFITPSQIAVENMSQCFENKKTFFVDS 300  
 Qy 301 DGSFPLSKLTVKDSRMOQGNVFCFSVMEHLAHNHTQKLSLSRCK 347  
 Db 301 DGSFPLSKLTVKDSRMOQGNVFCFSVMEHLAHNHTQKLSLSRCK 347

RESULT 4  
 US-09-734-300-9



CURRENT FILING DATE: 2002-04-11  
 PRIOR FILING DATE: 1999-09-22 / 05/9/22045  
 NUMBER OF SEQ ID NOS: 52  
 SEQ ID NO 1: Patent in version 3.0  
 SEQ ID NO 26  
 LENGTH: 1158  
 ORGANISM: Homo sapiens  
 US-09-935-868-26

Query Match  
 Best Local Similarity 79.3%; Score 1249; DB 9; Length 1158;  
 Matches 242; Conservative 11; Mismatches 30; Indels 22; Gaps 3;  
 Oy 65 ELNSEFAFSSR-----KNVLDVSGSLTVMITSSO-----EDYEMSP 108  
 Db 854 DUNGTINFTFTTIGMETAVWDSHSHTTSLSDTLVYHMAATDGGKGP 913  
 Oy 109 NITKMFY-----VQKTCPCAPPELLGSGVFLPPKPKOTMISRTPEVTCV 162  
 Db 914 EFTTTTFAQIESGDGATTCPCAPPELLGSGVFLPPKPKOTMISRTPEVTCV 973  
 Oy 163 VVNSHEDPCKFNKYVGVYVNNATKPREQVNSTVRSVSLVHQMCKREYCK 222  
 Db 974 VVNSHEDPCKFNKYVGVYVNNATKPREQVNSTVRSVSLVHQMCKREYCK 1033  
 Oy 223 IIVVNSHEDPCKFNKYVGVYVNNATKPREQVNSTVRSVSLVHQMCKREYCK 282  
 Db 1034 VNSKALPAPERTISKAGQPEKPVTLPSRDELTKNKGSLVCLVGFPSDIAYNE 1093  
 Oy 283 SNOQENPNKVTTPVLDSDGFFLSKLTYSKQSQGNQFSCSYNHEALNNITOKSL 342  
 Db 1094 SNOQENPNKVTTPVLDSDGFFLSKLTYSKQSQGNQFSCSYNHEALNNITOKSL 1153  
 Oy 343 LSPCK 347  
 Db 1154 LSPCK 1158

RESULT 6  
 US-09-935-868-24  
 : Sequence 24, Application US/0933868  
 : Patent No. US20020164650A1  
 : APPLICANT: Regeneron Pharmaceuticals, Inc  
 : TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using  
 : CURRENT APPLICATION NUMBER: US/09/935,868  
 : CURRENT FILING DATE: 2002-04-11  
 : PRIOR FILING DATE: 1999-09-22 / 05/9/22045  
 : NUMBER OF SEQ ID NOS: 52  
 : SEQ ID NO 1: Patent in version 3.0  
 : LENGTH: 1168  
 : ORGANISM: Homo sapiens  
 US-09-935-868-24

Query Match  
 Best Local Similarity 79.3%; Score 1249; DB 9; Length 1168;  
 Matches 242; Conservative 11; Mismatches 30; Indels 22; Gaps 3;  
 Oy 65 ELNSEFAFSSR-----KNVLDVSGSLTVMITSSO-----EDYEMSP 108  
 Db 864 DUNGTINFTFTTIGMETAVWDSHSHTTSLSDTLVYHMAATDGGKGP 923  
 Oy 109 NITKMFY-----VQKTCPCAPPELLGSGVFLPPKPKOTMISRTPEVTCV 162  
 Db 934 EFTTTTFAQIESGDGATTCPCAPPELLGSGVFLPPKPKOTMISRTPEVTCV 983  
 Oy 163 VVNSHEDPCKFNKYVGVYVNNATKPREQVNSTVRSVSLVHQMCKREYCK 222

Db 984 VVNSHEDPCKFNKYVGVYVNNATKPREQVNSTVRSVSLVHQMCKREYCK 1043  
 Oy 223 VNSKALPAPERTISKAGQPEKPVTLPSRDELTKNKGSLVCLVGFPSDIAYNE 282  
 Db 1044 VNSKALPAPERTISKAGQPEKPVTLPSRDELTKNKGSLVCLVGFPSDIAYNE 1103  
 Oy 283 SNOQENPNKVTTPVLDSDGFFLSKLTYSKQSQGNQFSCSYNHEALNNITOKSL 342  
 Db 1104 SNOQENPNKVTTPVLDSDGFFLSKLTYSKQSQGNQFSCSYNHEALNNITOKSL 1163  
 Oy 343 LSPCK 347  
 Db 1164 LSPCK 1168  
 RESULT 9  
 US-09-875-338-17  
 : Application US/09875338  
 : Patent No. US20020095024A1  
 : GENERAL INFORMATION: CHANG, HAN  
 : APPLICANT: CHANG, HAN  
 : APPLICANT: FINGER, JOSHUA N.  
 : APPLICANT: FINGER, JOSHUA N.  
 : APPLICANT: LIU, PIN  
 : APPLICANT: ZHOU, XIA-DI  
 : TITLE OF INVENTION: IMMUNOMODULATION  
 : FILE REFERENCE: 3053-4071US2  
 : CURRENT FILING DATE: 2001-06-06  
 : PRIOR APPLICATION NUMBER: 60/2772,107  
 : PRIOR FILING DATE: 2001-06-06  
 : PRIOR APPLICATION NUMBER: 60/209,811  
 : PRIOR FILING DATE: 2000-06-06  
 : NUMBER OF SEQ ID NOS: 94  
 : SOFTWARE: BIO ACID Ver. 2.1  
 : SEQ ID NO 17  
 : LENGTH: 451  
 : ORGANISM: Artificial Sequence  
 : FEATURE: CONFORMATION: Description of Artificial Sequence: Synthetic  
 : OTHER INFORMATION: Fusion Construct  
 US-09-875-338-17

Query Match  
 Best Local Similarity 70.1%; Score 1247; DB 10; Length 451;  
 Matches 253; Conservative 8; Mismatches 40; Indels 60; Gaps 6;  
 Oy 33 TGVV-----GVNTHFV-----PSNVLEKLVK-----58  
 Db 105 TGVV-----GVNTHFV-----PSNVLEKLVK-----58  
 Oy 59 -----QOKVNLNDEFAFSSFNRYVDTSSGLT-----VNTSSDDEDETE 106  
 Db 165 SHTSFELGVDTSLVGLPCKPNSG-----VVNTHVETLTASLDSDDEPETER 220  
 Oy 167 SHTSFELGVDTSLVGLPCKPNSG-----VVNTHVETLTASLDSDDEPETER 220  
 Oy 221 PHS-----CQHTKPCPCAPPELLGSGVFLPPKPKOTMISRTPEVTCV 270  
 Db 167 SHTSFELGVDTSLVGLPCKPNSG-----VVNTHVETLTASLDSDDEPETER 220  
 Oy 271 SHTSFELGVDTSLVGLPCKPNSG-----VVNTHVETLTASLDSDDEPETER 220  
 Db 271 SHTSFELGVDTSLVGLPCKPNSG-----VVNTHVETLTASLDSDDEPETER 220  
 Oy 331 ALPAPERTISKAGQPEKPVTLPSRDELTKNKGSLVCLVGFPSDIAYNE 390  
 Db 287 PENNYKVTTPVLDSDGFFLSKLTYSKQSQGNQFSCSYNHEALNNITOKSL 346

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Db 391 PENKKTTPVVDVSGSFLLKLVKVKSHMOQGNFSCSYHMEALNNHTOKSLASPG 430
Oy 347 K 347
Db 451 K 451

RESULT 10
: Sequence 9
: Sequence 9: Application US/09875338
: PATENT INFORMATION:
: Patent No. US20020095024A1
: APPLICANT: HERGENSON, GLEN E.
: APPLICANT: HERGENSON, GLEN E.
: APPLICANT: FINGER, JOSHUA N.
: APPLICANT: FINGER, JOSHUA N.
: APPLICANT: LIU, PIN
: APPLICANT: ZHOU, XIA-DI
: TITLE OF INVENTION: 87-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
: FILE REFERENCE: IMMUNOMODULATION
: FILE REFERENCE: 103-4071062 US/09/875,338
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 60/272,107
: PRIOR FILING DATE: 2000-06-06
: PRIOR APPLICATION NUMBER: 60/209,811
: PRIOR FILING DATE: 2000-06-06
: SOFTWARE: PARADIGM Ver. 2.1
: SEQ ID NO 9
: LENGTH: 698
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Fusion Construct
: US-09-875-338-9

Query Match 67.4%; Score 1247; Db 10; Length 698;
Best Local Similarity 87.4%; Pred. No. 2.2e-80;
Matches 216; Conservative 5; Mismatches 17; Indels 12; Gaps 1;

Db 78 KRWVLTQVSGSLTVNLSSDEDEYHMSNITOMKFTVYKTHCPCPAPBLGG 137
Oy 441 RWVLDQMSGSLTVITQTPPEPERS
Db 138 PSVFLPFRKPTKMTISRTPEVTVYVDSHDEYKFNMYGVGVHMAKTPREQDIN 197
Oy 489 PSVFLPFRKPTKMTISRTPEVTVYVDSHDEYKFNMYGVGVHMAKTPREQDIN 548
Oy 198 STSRKGVVTVYVQVQKGVKGVKYNKALPAKPTKTSKAGQRPQVTLPSDE 257
Oy 549 STYVNSVTVYVQVQKGVKGVKYNKALPAKPTKTSKAGQRPQVTLPSDE 608
Oy 258 LTKNVLGCLVTKGVTSADVNSGQPNPKTKTPPVVDVSGSFLLKLVKVKSH 317
Db 609 LTKNVLGCLVTKGVTSADVNSGQPNPKTKTPPVVDVSGSFLLKLVKVKSH 668
Oy 318 QGVNFGSCSYHMEALNNHTOKSLASPG 347
Db 669 QGVNFGSCSYHMEALNNHTOKSLASPG 698

RESULT 11
: Sequence 16
: Sequence 16: Application US/0974623
: PATENT INFORMATION:
: Patent No. US2002009454A1
: APPLICANT: HERGENSON, GLEN E.
: APPLICANT: BOONE, THOMAS C.
: APPLICANT: HERGENSON, SUSAN
: APPLICANT: BEVILACQUA, MICHAEL P.

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: APPLICANT: COLLINS, DAVID S.
: TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING INFLAMMATORY
: DISEASES
: CURRENT APPLICATION NUMBER: US/09/784,623
: CURRENT FILING DATE: 2001-02-15
: PRIOR APPLICATION NUMBER: US/09/784,623
: PRIOR FILING DATE: 1998-08-07
: PRIOR APPLICATION NUMBER: PCT/US 97/02131
: PRIOR FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentLin Ver. 2.0
: SEQ ID NO 16
: TYPE: PRT
: ORGANISM: Human
: US-09-784-623-16

Query Match 66.9%; Score 1242; Db 10; Length 388;
Best Local Similarity 84.9%; Pred. No. 1.1e-76;
Matches 249; Conservative 16; Mismatches 30; Indels 88; Gaps 5;

Oy 30 QVTVGVGVTVFVNSVPLKRYAKKKQVAKLNSERAFSSFNKNVYLYDYS 89
Db 25 NQVAVAGLQ-----PNNVLE-----KIDWFE-----PFAFLGIRGG 65
Oy 90 LTTKNSGDSGRTSPNSGRTSDM-----REFVY----- 120
Db 66 KLSGKSGDGTETALQVAVITDLSNKKQKRAEFTSFESACQNFCTA 125
Oy 121 ----- 144
Db 126 MSADVPLSLNPDQGVWYKTFYQDGAANAAPRSQKTHCPCPAPBLGGSVLP 185
Oy 145 FKPTKMTISRTPEVTVYVDSHDEYKFNMYGVGVHMAKTPREQDINSTRV 204
Db 186 FKPTKMTISRTPEVTVYVDSHDEYKFNMYGVGVHMAKTPREQDINSTRV 245
Oy 205 VLVVQHQKSKETCKYKNAKALPAKPTKTSKAGQRPQVTLPSDELTNQS 264
Db 246 VLVVQHQKSKETCKYKNAKALPAKPTKTSKAGQRPQVTLPSDELTNQS 305
Oy 245 LKGVNFGSCSYHMEALNNHTOKSLASPG 347
Db 306 LKGVNFGSCSYHMEALNNHTOKSLASPG 365
Oy 325 CSYHMEALNNHTOKSLASPG 347
Db 366 CSYHMEALNNHTOKSLASPG 388

RESULT 12
: Sequence 3
: Sequence 3: Application US/09845899A
: PATENT INFORMATION:
: Patent No. US2002014732A1
: APPLICANT: WANCY ANN
: APPLICANT: LIN, SALLY DOREEN PATRICIA
: APPLICANT: SHERT, RAYMOND W.
: APPLICANT: SHERT, RAYMOND W.
: TITLE OF INVENTION: HEXAMERIC
: TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/845,899A
: CURRENT FILING DATE: 2001-04-30
: PRIOR APPLICATION NUMBER: US/09/202,346
: PRIOR APPLICATION NUMBER: US 60/043,948
: PRIOR FILING DATE: 1997-02-19
: PRIOR FILING DATE: 1997-02-19
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: FastSD for Windows Version 3.0

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; SEQ ID NO 2
; NAME: PRT
; TYPE: PRT
; ORGANISM: RHO SNIENS
US-09-843-839-2
Query Match
  66.9% Score 1240; DB 10; Length 492;
  95.2% Identity 39.2% Pos. 3, 4e-80
  250 Conservative 14; Mismatches 56; Indels 122; Gaps
5;

Oy 48 NPTLE-----VLMKKDKVMELEDEAFKSFSEKRVLYTQSG-SLTNYTSSDD 101
Db 53 NVSEVLAOTRIYQKIKKVIYTWSDGMINIFPKTRIFIDITNNLSVILALRFSDD 112
Oy 102 EYE-----NESP----- 108
Db 113 TTYCTVATKDAFRIHARVTLGVADPTFSDIFPSIHRICITSGSGDPEH 172
Oy 109 -----NLTDMKSFVL----- 120
Db 173 LSHIEEELAMINTVSDPELTAVLSKLDKNTFMSKLCIKGLHVAQFQNM 232
Oy 121 -----DRTHTCPAPFELGDSVFLPKPKDTMISRTPEVTCVVD 165
Db 233 TTQHQEPQDSKSHATHTCPAPFELGDSVFLPKPKDTMISRTPEVTCVVD 292
Oy 166 VSEDEPKMTVYGVENNAKTPREDTNSTRVSLTVTADQMLNKEKCKVSN 225
Db 235 VSEDEPKMTVYGVENNAKTPREDTNSTRVSLTVTADQMLNKEKCKVSN 352
Oy 226 KALPAPKRTISKAGQRPBPQVTLPSKRGKQVLSKLVKSLVYKQVSNVNSK 285
Db 353 KALPAPKRTISKAGQRPBPQVTLPSKRGKQVLSKLVKSLVYKQVSNVNSK 412
Oy 286 OPENNYKTPPVLDSGDSFLSKLTVKSGWQGVFCFSVMEALJNHITQKLSLP 345
Db 413 OPENNYKTPPVLDSGDSFLSKLTVKSGWQGVFCFSVMEALJNHITQKLSLP 472
Oy 346 GK 347
Oy 473 GK 474

RESUME 13
US-09-832-659-2
; Sequence 2, Application US/09812659
; Patent No. US20020015547A1
; GENE: INTERFERON-BETA
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Interferon-Beta Fusion Proteins and Uses
; CURRENT FILING DATE: 2001-04-11
; PRIOR FILING DATE: 1999-02-10/210,237
; PRIOR APPLICATION NUMBER: 60/104,491
; NUMBER OF SEQ ID NOS: 199-10-16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 359
; NAME: PRT
; TYPE: PRT
; ORGANISM: murine
US-09-832-659-2
Query Match
  66.8% Score 1240; DB 9; Length 399;
  95.2% Identity 39.2% Pos. 3, 4e-80
  233 Conservative 9; Mismatches 6; Indels 22; Gaps
2;

Oy 78 NRVLYTVSSGLTVTVTSSDDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 137
Db 152 NRVLYTVSSGLTVTVTSSDDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 199
Db 152 NRVLYTVSSGLTVTVTSSDDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 214

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Oy 180 DOVEYHNATKFERQDINSTVWVSVLVHDOMLNKRETKCKYSNKLAPARTKETSIA 239
Db 315 DOVEYHNATKFERQDINSTVWVSVLVHDOMLNKRETKCKYSNKLAPARTKETSIA 374
Oy 240 KQDPERQVTLTPSRBELTKNOVSLCGLKGFYPSDIAVWMSNOGPNNTKTFPVLD 299
Db 375 KQDPERQVTLTPSRBELTKNOVSLCGLKGFYPSDIAVWMSNOGPNNTKTFPVLD 434
Oy 300 SDGSFELYSKLVKYSKMOQGNVPSVWHEALJHNKTSLSLSPCK 347
Db 435 SDGSFELYSKLVKYSKMOQGNVPSVWHEALJHNKTSLSLSPCK 482

RESULT 15
US-09-730-465-8-20
Sequence 20, Application US/09935868
Patent No. US2002016490A1
GENERAL INFORMATION:
GEOGRAPHIC INFORMATION:
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 2018P, US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIORITY DATE: 1999-09-22
NUMBER OF SEQ IDS NOS: 95
SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; Length: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-20

Query Match
RefSeq Loc. Similarity 66.7%; Score 1238.5; DB 9; Length 651;
RefSeq Accession: U00001.1; Pred. No. 84e-001;
Matches 248; Conservative 10; Mismatches 58; Indels 51; Gaps 6;

Oy 39 GNTVTRV-----PNTPLARY-----LAKQKD-----KVADLNSER 72
Db 358 GNLTHWNSDITLLNSPVPDNLVHLYTVANNSENADPRTVNTVLEPSIRI 417
Oy 73 NRSKRWV-LUTYSSSITINLSE-----ELVTKSSPMDTKKFLV 120
Db 418 AASTLSGLSTYARVNAAGSNTTWSEKSPKTHNISTYBEPFQGG----- 464
Oy 121 KNTWTCPCPAPELLGDSVFLPPEKPTLMISRTPTCTCVVNSHEDPVRKMYND 180
Db 465 DNTWTCPCPAPELLGDSVFLPPEKPTLMISRTPTCTCVVNSHEDPVRKMYND 524
Oy 181 GVEYHNATKFERQDINSTVWVSVLVHDOMLNKRETKCKYSNKLAPARTKETSIAK 240
Db 525 GVEYHNATKFERQDINSTVWVSVLVHDOMLNKRETKCKYSNKLAPARTKETSIAK 584
Oy 241 GQDPERQVTLTPSRBELTKNOVSLCGLKGFYPSDIAVWMSNOGPNNTKTFPVLD 300
Db 585 GQDPERQVTLTPSRBELTKNOVSLCGLKGFYPSDIAVWMSNOGPNNTKTFPVLD 644
Oy 301 DSDFELYSKLVKYSKMOQGNVPSVWHEALJHNKTSLSLSPCK 347
Db 645 DSDFELYSKLVKYSKMOQGNVPSVWHEALJHNKTSLSLSPCK 691

Search completed: January 28, 2003, 08:53:01
Job time : 114.923 secs

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i. MOLECULE TYPE: protein
US-07-940-861-43

Query Match
Best Local Similarity 100.0%; Score 1856; DB 1; Length 347;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Db 1 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Oy 61 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Db 61 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Oy 121 DKHTPCPCAPFELGSGSVLPFKPKKDLMIERTFETVGVVDSDEDESPNITDKMFELV 120
Db 121 DKHTPCPCAPFELGSGSVLPFKPKKDLMIERTFETVGVVDSDEDESPNITDKMFELV 120
Oy 181 GYVWNAATKPREQVNTVRSVLTVLVHQMKGKCKVSKNKALEPTEKTSKAK 240
Db 181 GYVWNAATKPREQVNTVRSVLTVLVHQMKGKCKVSKNKALEPTEKTSKAK 240
Oy 241 GQPEPVYTLPPFSRDELTNKSLSCLVKGTPSDVAKMNSQGFENKATTPPVLD 300
Db 241 GQPEPVYTLPPFSRDELTNKSLSCLVKGTPSDVAKMNSQGFENKATTPPVLD 300
Oy 301 GDSFPLYSKLTVDKSRWQGVFSCSVMHAEALNHHTQKLSLSPOK 347
Db 301 GDSFPLYSKLTVDKSRWQGVFSCSVMHAEALNHHTQKLSLSPOK 347

RESULT 2
US-08-459-657-43
GENERAL INFORMATION:
Patent No. 5728677
Application US/08459512
APPLICANT: BIONEER, INC.
APPLICANT: MILLER, Glenn T.
APPLICANT: WALLNER, Barbara P.
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES 43
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
CORRESPONDENCE ADDRESS:
STREET: 875 Third Avenue
ADDRESS: Fish & Neave
CITY: New York
STATE: New York
COUNTRY: U.S.A.
COMPUTER: IBM PC compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: PatentIn Release #11.0, Version #1.25
CURRENT APPLICATION DATA: 08/08/459.512
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE: 1551C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0660
TELEFAX: (212)715-0673
INVENTOR: WALLNER, Barbara P.
SEQUENCE CHARACTERISTICS
LENGTH: 347 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-459-512-43

Query Match
Best Local Similarity 100.0%; Score 1856; DB 1; Length 347;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Db 1 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Oy 61 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Db 61 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Oy 121 DKHTPCPCAPFELGSGSVLPFKPKKDLMIERTFETVGVVDSDEDESPNITDKMFELV 120
Db 121 DKHTPCPCAPFELGSGSVLPFKPKKDLMIERTFETVGVVDSDEDESPNITDKMFELV 120
Oy 181 GYVWNAATKPREQVNTVRSVLTVLVHQMKGKCKVSKNKALEPTEKTSKAK 240
Db 181 GYVWNAATKPREQVNTVRSVLTVLVHQMKGKCKVSKNKALEPTEKTSKAK 240
Oy 241 GQPEPVYTLPPFSRDELTNKSLSCLVKGTPSDVAKMNSQGFENKATTPPVLD 300
Db 241 GQPEPVYTLPPFSRDELTNKSLSCLVKGTPSDVAKMNSQGFENKATTPPVLD 300
Oy 301 GDSFPLYSKLTVDKSRWQGVFSCSVMHAEALNHHTQKLSLSPOK 347
Db 301 GDSFPLYSKLTVDKSRWQGVFSCSVMHAEALNHHTQKLSLSPOK 347

US-08-459-657-43
GENERAL INFORMATION:
Patent No. 5914111
Application US/08459657
APPLICANT: BIONEER, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: RUSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES 43
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
CORRESPONDENCE ADDRESS:
STREET: 875 Third Avenue
ADDRESS: Fish & Neave
CITY: New York
STATE: New York
COUNTRY: U.S.A.
COMPUTER: IBM PC compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: PatentIn Release #11.0, Version #1.25
CURRENT APPLICATION DATA: 08/08/459.657
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE: 1551C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0660
TELEFAX: (212)715-0673
INVENTOR: WALLNER, Barbara P.
SEQUENCE CHARACTERISTICS
LENGTH: 347 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-459-512-43

Query Match
Best Local Similarity 100.0%; Score 1856; DB 1; Length 347;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Db 1 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Oy 61 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Db 61 DWASDGRALGVLYVCLLCRCPCICFSCQITGVGVNTFWFVSNVPLVLAKKQK 60
Oy 121 DKHTPCPCAPFELGSGSVLPFKPKKDLMIERTFETVGVVDSDEDESPNITDKMFELV 120
Db 121 DKHTPCPCAPFELGSGSVLPFKPKKDLMIERTFETVGVVDSDEDESPNITDKMFELV 120
Oy 181 GYVWNAATKPREQVNTVRSVLTVLVHQMKGKCKVSKNKALEPTEKTSKAK 240
Db 181 GYVWNAATKPREQVNTVRSVLTVLVHQMKGKCKVSKNKALEPTEKTSKAK 240
Oy 241 GQPEPVYTLPPFSRDELTNKSLSCLVKGTPSDVAKMNSQGFENKATTPPVLD 300
Db 241 GQPEPVYTLPPFSRDELTNKSLSCLVKGTPSDVAKMNSQGFENKATTPPVLD 300
Oy 301 GDSFPLYSKLTVDKSRWQGVFSCSVMHAEALNHHTQKLSLSPOK 347
Db 301 GDSFPLYSKLTVDKSRWQGVFSCSVMHAEALNHHTQKLSLSPOK 347

```



```

1 CITY: Boston
2 STATE: Massachusetts
3 COUNTRY: USA
4 COUNTRY: 100.00%
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: PatentIn Release #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 FILING DATE: US/09/466,465
12 PRIORITY NUMBER:
13 FILING DATE:
14 PRIOR APPLICATION DATA:
15 FILING DATE: US/09/392,007/5
16 PRIOR APPLICATION DATA:
17 FILING DATE: US-OCT-1992
18 APPLICATION NUMBER: US 07/862,022
19 PRIOR APPLICATION DATA:
20 FILING DATE:
21 APPLICATION NUMBER: US 07/770,969
22 PRIOR APPLICATION DATA:
23 FILING DATE:
24 NAME: Myers, Louis (PLM)
25 ADDRESS:
26 REFERENCE/DOCKET NUMBER: 969
27 TELECOMMUNICATION INFORMATION:
28 NAME: NALEY, James F.
29 TELEPHONE: (617) 227-7400
30 INFORMATION FOR SEQ ID NO: 1:
31 SEQUENCE CHARACTERISTICS:
32 TYPE: amino acid
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35 US-08-465-403-8
36
37 Query Match 100.0%; Score 1856; DB 4; Length 347;
38 Best Local Similarity 100.0%; Pred. No. 3, 26-163;
39 Matches 347; Conservative 0; Mismatches 0; Indels 0; Caps 0;
40
41 QY 1 KWAGSDAGALGVSLVCLKRFQISCSQQITGVGYNTFVFNPLKVKKK 60
42 DB 1 KWAGSDAGALGVSLVCLKRFQISCSQQITGVGYNTFVFNPLKVKKK 60
43
44 QY 61 DWALENSFPAFSKFNRYVLTGVSLTYLTLSSDEEYDMSPTDMKFFLY 120
45 DB 61 DWALENSFPAFSKFNRYVLTGVSLTYLTLSSDEEYDMSPTDMKFFLY 120
46
47 QY 121 DKHTCPCPAFELGDSVFFPPFKPOTLMSRFTVGVVSHEDPEKNVYD 180
48 DB 121 DKHTCPCPAFELGDSVFFPPFKPOTLMSRFTVGVVSHEDPEKNVYD 180
49
50 QY 181 GVEVNNATKPREQYNTSVYSLVYLHQWJGKEVCKVSKALPAETKTSK 240
51 DB 181 GVEVNNATKPREQYNTSVYSLVYLHQWJGKEVCKVSKALPAETKTSK 240
52
53 QY 241 GQRPFOVTLPPSRDELTKNOVSLTCLVGYTFSDIAYVMSHQPNNTKTPV 300
54 DB 241 GQRPFOVTLPPSRDELTKNOVSLTCLVGYTFSDIAYVMSHQPNNTKTPV 300
55
56 QY 301 DGSFTLYSLTKVNSKQGNQVFCSSVMEALHHNTKSLSPCK 347
57 DB 301 DGSFTLYSLTKVNSKQGNQVFCSSVMEALHHNTKSLSPCK 347
58
59 RESULT 6
60 PCT-US92-02050-43
61 : Application US/09-730-465-8-rai
62 : General Information:
63 : APPLICANT: BIOGEN, INC.
64 : APPLICANT: WALLACE, Margaret A.
65 : APPLICANT: ROSA, Margaret D.
66
67 TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCTE
68 TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
69 NUMBER OF SEQUENCES: 43
70 COUNTRY: 100.00%
71 ADDRESS: Fish & Neave
72 STREET: 875 Third Avenue
73 CITY: New York
74 STATE: New York
75 COUNTRY: U.S.A.
76 ZIP: 10022-6325
77 FORM:
78 MEDIUM TYPE: Floppy disk
79 COMPUTER: IBM PC compatible
80 SOFTWARE: PatentIn Release #1.0, Version #1.25
81 CURRENT APPLICATION DATA:
82 FILING DATE: US/09/466,465
83 PRIORITY NUMBER: PCT/US92/02050
84 CLASSIFICATION: 435
85 PRIOR APPLICATION DATA: US 07/467,971
86 FILING DATE: 12-MAR-1991
87 PRIOR APPLICATION DATA: US 07/770,967
88 FILING DATE: 07-OCT-1991
89 ATTORNEY/AGENT INFORMATION:
90 REFERENCE/DOCKET NUMBER: B15C1P2
91 TELECOMMUNICATION INFORMATION:
92 NAME: NALEY, James F.
93 TELEPHONE: (617) 227-7400
94 INFORMATION FOR SEQ ID NO: 2:
95 SEQUENCE CHARACTERISTICS:
96 TYPE: amino acid
97 TOPOLOGY: linear
98 MOLECULE TYPE: protein
99 US-08-465-403-8
100
101 Query Match 100.0%; Score 1856; DB 5; Length 347;
102 Best Local Similarity 100.0%; Pred. No. 3, 26-163;
103 Matches 347; Conservative 0; Mismatches 0; Indels 0; Caps 0;
104
105 QY 1 KWAGSDAGALGVSLVCLKRFQISCSQQITGVGYNTFVFNPLKVKKK 60
106 DB 1 KWAGSDAGALGVSLVCLKRFQISCSQQITGVGYNTFVFNPLKVKKK 60
107
108 QY 61 DWALENSFPAFSKFNRYVLTGVSLTYLTLSSDEEYDMSPTDMKFFLY 120
109 DB 61 DWALENSFPAFSKFNRYVLTGVSLTYLTLSSDEEYDMSPTDMKFFLY 120
110
111 QY 121 DKHTCPCPAFELGDSVFFPPFKPOTLMSRFTVGVVSHEDPEKNVYD 180
112 DB 121 DKHTCPCPAFELGDSVFFPPFKPOTLMSRFTVGVVSHEDPEKNVYD 180
113
114 QY 181 GVEVNNATKPREQYNTSVYSLVYLHQWJGKEVCKVSKALPAETKTSK 240
115 DB 181 GVEVNNATKPREQYNTSVYSLVYLHQWJGKEVCKVSKALPAETKTSK 240
116
117 QY 241 GQRPFOVTLPPSRDELTKNOVSLTCLVGYTFSDIAYVMSHQPNNTKTPV 300
118 DB 241 GQRPFOVTLPPSRDELTKNOVSLTCLVGYTFSDIAYVMSHQPNNTKTPV 300
119
120 QY 301 DGSFTLYSLTKVNSKQGNQVFCSSVMEALHHNTKSLSPCK 347
121 DB 301 DGSFTLYSLTKVNSKQGNQVFCSSVMEALHHNTKSLSPCK 347
122
123 RESULT 7
124 PCT-US92-02050-43
125 : Application US/09-730-465-8-rai
126 : General Information:
127 : APPLICANT: BIOGEN, INC.
128 : APPLICANT: WALLACE, Margaret A.
129 : APPLICANT: ROSA, Margaret D.

```







Oy 166 VSHEDPDKVNTVGVGVNHNATKREDOVNSTVNVSVTVLQDLMKTKCKVSN 225  
 Db 256 VSHEDPDKVNTVGVGVNHNATKREDOVNSTVNVSVTVLQDLMKTKCKVSN 315  
 Oy 226 KALPAPTEKTSKAGOPPEVTVLPPSRDELTKNVSCLVKGYFSDAVRESNG 285  
 Db 316 KALPAPTEKTSKAGOPPEVTVLPPSRDELTKNVSCLVKGYFSDAVRESNG 375  
 Oy 286 OFENMNTTPPVLDSDGSFLVTLKVDKSHMOQGNFVSCYVHWEALNHNITOKSLSP 345  
 Db 376 OFENMNTTPPVLDSDGSFLVTLKVDKSHMOQGNFVSCYVHWEALNHNITOKSLSP 435  
 Oy 346 GK 347  
 Db 436 GK 437

## RESULT 14

: Sequence 15, Application US/0827496C  
 : GENERAL INFORMATION:  
 : APPLICANT: Greve, Jeffrey M.  
 : INVENTOR: Greve, Jeffrey M. and Alan  
 : TITLE OF INVENTION: Rhinovirus Receptor Protein  
 : NUMBER OF SEQUENCES: 20  
 : CLAIMS: 1  
 : ADDRESS: Bayer Corporation  
 : STREET: 400 Morgan Lane  
 : CITY: Connecticut  
 : STATE: Connecticut  
 : COUNTRY: USA  
 : ZIP: 06516  
 : COMPUTER: IBM compatible pcwv;  
 : MEDIUM TYPE: diskette, 1.44 Mb storage  
 : COMPUTER: Dell Optiplex GX1  
 : MEDIUM TYPE: hard disk  
 : SOFTWARE: Microsoft Windows  
 : CURRENT APPLICATION DATA:  
 : FILING DATE: 06/14/94  
 : FILING DATE: 06/14/94  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : FILING DATE: 07/09/069  
 : APPLICATION NUMBER: 07/704,984  
 : APPLICATION NUMBER: 07/558,238  
 : FILING DATE: 07/20/90  
 : FILING DATE: 07/20/90  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Barbara A. Skolnik  
 : REGISTRATION NUMBER: 29,862  
 : REFERENCE/DOCKET NUMBER: MPT 214, 2C  
 : TELEPHONE: (203) 812-2786  
 : TELEFAX: (203) 812-5492  
 : INFORMATION FOR SEQ ID NO: 15:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 680 amino acid residues  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : DESCRIPTION: complete  
 : FRAGMENT TYPE: complete sequence  
 : OTHER INFORMATION: LIGAND:182/199 fusion protein  
 : OTHER INFORMATION: amino acid residues 1-453 =  
 : OTHER INFORMATION: LIGAND(453): amino acid residues 454-680 = amino  
 : OTHER INFORMATION: acid residues 216-442 of human 19G1 heavy chain  
 US-08-227-486-15

Query Match 66.7%, Score 1239, DB 4; Length 680;  
 Best Local Similarity 95.6%; Pred. NO. 8, 6e-106;  
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 119 YDKTHKTPCCAPPELLGGPSVFLPPLKKPKCTALSTSTPEVGVVYSDPEVFNKK 178  
 Db 178 YDKTHKTPCCAPPELLGGPSVFLPPLKKPKCTALSTSTPEVGVVYSDPEVFNKK 178  
 Oy 432 YGVGVNHNATKREDOVNSTVNVSVTVLQDLMKTKCKVSNKALPAPTEKTSK 238  
 Db 432 YGVGVNHNATKREDOVNSTVNVSVTVLQDLMKTKCKVSNKALPAPTEKTSK 238  
 Oy 512 YGVGVNHNATKREDOVNSTVNVSVTVLQDLMKTKCKVSNKALPAPTEKTSK 571  
 Db 512 YGVGVNHNATKREDOVNSTVNVSVTVLQDLMKTKCKVSNKALPAPTEKTSK 571  
 Oy 239 AKGQREPVTVLPPSRDELTKNVSCLVKGYFSDAVRESNGOPENNKTPPVVL 298  
 Db 239 AKGQREPVTVLPPSRDELTKNVSCLVKGYFSDAVRESNGOPENNKTPPVVL 298  
 Oy 572 AKGQREPVTVLPPSRDELTKNVSCLVKGYFSDAVRESNGOPENNKTPPVVL 631  
 Db 572 AKGQREPVTVLPPSRDELTKNVSCLVKGYFSDAVRESNGOPENNKTPPVVL 631  
 Oy 299 DSDGSFLVKSLKVDKSHMOQGNFVSCYVHWEALNHNITOKSLSPK 347  
 Db 299 DSDGSFLVKSLKVDKSHMOQGNFVSCYVHWEALNHNITOKSLSPK 347  
 Oy 632 DSDGSFLVKSLKVDKSHMOQGNFVSCYVHWEALNHNITOKSLSPK 680  
 Db 632 DSDGSFLVKSLKVDKSHMOQGNFVSCYVHWEALNHNITOKSLSPK 680

## RESULT 15

: Sequence 2, Application US/0876511  
 : GENERAL INFORMATION:  
 : APPLICANT: Young, Peter R.  
 : INVENTOR: Young, Peter R.  
 : TITLE OF INVENTION: Method for Obtaining Receptor Agonist  
 : NUMBER OF SEQUENCES: 13  
 : CLAIMS: 13  
 : ADDRESS: SmithKline Beecham Corporation  
 : STREET: 900 Springwood Road  
 : CITY: King of Prussia  
 : STATE: Pennsylvania  
 : ZIP: 19406-7999  
 : COMPUTER: IBM compatible  
 : MEDIUM TYPE: floppy disk  
 : SOFTWARE: PC-DOS/MS-DOS  
 : CURRENT APPLICATION DATA:  
 : FILING DATE: 08/08/93  
 : FILING DATE: 08/08/93  
 : APPLICATION NUMBER: US/08/776,511  
 : PRIOR APPLICATION DATA:  
 : FILING DATE: 08/08/93  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Jervis, Herbert H.  
 : REGISTRATION NUMBER: 31,174  
 : REFERENCE/DOCKET NUMBER: PRC P50349-1  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 610-270-5015  
 : INFORMATION FOR SEQ ID NO: 2:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 488 amino acids  
 : TYPE: amino acids  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : DESCRIPTION: protein  
 : FRAGMENT TYPE: protein  
 US-08-776-511-1

Query Match 66.6%, Score 1235.5, DB 4; Length 488;  
 Best Local Similarity 95.6%; Pred. NO. 8, 6e-106;  
 Matches 234; Conservative 1; Mismatches 11; Indels 7; Gaps 2;

Oy 95 LTSSDEDEYEMSPHITDMFVLKTVKTPCCAPPELLGGPSVFLPPLKKPKLMTLS 154  
 Db 243 LTSSDEDEYEMSPHITDMFVLKTVKTPCCAPPELLGGPSVFLPPLKKPKLMTLS 295  
 Oy 155 WTSPVGVGVVYSDPEVFNKKPKCTALSTSTPEVGVVYSDPEVFNKKPKLMTLS 214  
 Db 155 WTSPVGVGVVYSDPEVFNKKPKCTALSTSTPEVGVVYSDPEVFNKKPKLMTLS 214



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DB 206 RTEYTCVVYVSHEDPEVKFNWYDGVYHNATKPREQYNSTRVYSWZYLJQDWL 355
OY 215 NQKQKCVSNWALJATKERTISKANDQSRQWTEPQSDQFKNQVSLRCLVGGFP 274
DB 356 NQKQKCVSNWALJATKERTISKANDQSRQWTEPQSDQFKNQVSLRCLVGGFP 415
OY 275 SDIANVMSHQCPNNYKTPPYLDSQCSFLYSLTVKSNMOQWFSQWHAJLN 334
DB 416 SDIANVMSHQCPNNYKTPPYLDSQCSFLYSLTVKSNMOQWFSQWHAJLN 475
OY 335 HTQKSLSLSPK 347
DB 476 HTQKSLSLSPK 488

```

Search completed: January 28, 2003, 08:40:11  
 Job time : 17.0315 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Comogen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2003, 08:45:45 - Search time 14 seconds  
(without alignments)  
109,968 Million cell updates/sec

Title: US-09-730-465-2\_COPY\_50\_65

Sequence score:

Sequence: 1 PLEUYLVKKQKVAL 16

Scoring table: RMOSUMS

GapP 10.0 - Gapext 0.5

Searched: 281224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

pred. No. is the number of results predicted by chance to have a  
score of 1 or higher. The number of results actually printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	28	33.3	12	2 S69123
2	25	32.1	14	2 A35445
3	24	28.6	13	2 P00445
4	24	28.6	13	2 P00445
5	24	28.6	15	2 S36888
6	23	27.4	15	2 S36888
7	23	27.4	15	2 S32140
8	23	27.4	15	2 S21202
9	22	26.2	15	2 S21202
10	22	26.2	15	2 S21202
11	21	25.0	9	2 A60356
12	21	25.0	13	2 S60046
13	21	25.0	13	2 S60046
14	21	25.0	15	2 S33781
15	21	25.0	15	2 S33781
16	20	23.8	10	2 P00116
17	20	23.8	10	2 P00116
18	20	23.8	10	2 P00116
19	20	23.8	12	2 S50233
20	20	23.8	12	2 S50233
21	20	23.8	14	2 S60414
22	20	23.8	14	2 S60414
23	20	23.8	14	2 S60414
24	20	23.8	14	2 S60414
25	20	23.8	14	2 S60414
26	20	23.8	14	2 S60414
27	20	23.8	14	2 S60414
28	20	23.8	16	2 A23446
29	19	22.6	12	2 S58273

histone H1.c - mou  
histone H1a - mou  
histone H1b - mou  
hemoglobin beta ch  
fructose-bisphosph  
7 alpha-hydroxy-4-  
homocyst protein G  
mestran B - hor  
probable trypsin  
probable trypsin  
gene HXA protein  
lactate phosphatase  
proteasome subunit  
Ig H chain V-D-J r

## ALIGNMENTS

RESULT 1  
C:Species: Rhodospirillum rubrum (fragment)  
C:Accession: S69123  
C:Date: 10-Mar-1996  
R:Biopig, C.; Bolton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.  
R:Date: 10-Mar-1996  
A:Reference number: S69123  
A:Accession: S69123  
A:Structure: Preliminary  
A:Residues: 1-12  
Query Match 33.3% Score 28; DB 2: Length 12;  
Best Local Similarity 50.0%; Pred. No. 2, 2, 5, 0, 0;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Query Match 33.3% Score 28; DB 2: Length 12;  
Best Local Similarity 50.0%; Pred. No. 2, 2, 5, 0, 0;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Oy 4 EVLVKKQK 11  
Db 3 DVMWVOR 10  
:::1:1  
:::1:1  
:::1:1

RESULT 2  
C:Species: Escherichia coli (fragment)  
C:Accession: S14945  
R:Bio, T.; Bourne, J.C.; Blumenthal, R.M.  
A:Reference number: S14945  
A:Accession: S14945  
A:Structure: Preliminary  
A:Residues: 1-14  
Query Match 32.1% Score 27; DB 2: Length 14;  
Best Local Similarity 45.5%; Pred. No. 2, 2, 5, 0, 0;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Oy 2 LEVYVKKQK 12  
Db 1 LEVYVKKQK 11  
:::1:1  
:::1:1  
:::1:1

RESULT 3  
C:Species: Clostridium stick  
glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium stick





```

Db: 3 MKK 5

RESULT 14
S33781
C:Enzyme: acetate synthase (SF 4.1.3.18) large chain, valine-sensitive - Serratia marcescens
C:Species: Serratia marcescens
C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: G45681
C:Author: J.H. Kim, S.S. Yang
Biochim. Biophys. Acta 1157, 178-184, 1993
A:Title: Purification and characterization of the valine sensitive acetoacetate synthase
A:Accession: S33781
A:Accession: S33781, M519328309, PMID:937653
A:Molecule types: protein
A:Experimental source: ATCC 25419
C:Complex: heterotrimer: two small and two large chains
A:Pathway: valine, leucine, and isoleucine biosynthesis
A:Pathway: valine, leucine, and isoleucine biosynthesis
A:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; H
Query Match 25.0% Score 21; DB 2; Length 15;
Best Local Similarity 50.0% Prod. No. 4, 2e-03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy: 7 MKKQKD 12
Db: 5 MNQQLD 14

RESULT 15
Query Match 61.1 - phase T6 (fragment)
Best Local Similarity 61.1 - phase T6 (fragment)
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy: 61.1 - phase T6 (fragment)
Db: 5 MNQQLD 14

RESULT 16
C:Species: phase T6
C:Accession: G45681
C:Author: R. Selick, H.E.; Stormo, G.D.; Dyson, R.L.; Alberts, B.M.
J. Mol. Biol. 271, 2105-2116, 1993
A:Title: A yeast suppressive protein-coding sequence clustered between the pro
A:Reference number: M45681; M519328309; PMID:838243
A:Accession: G45681
A:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; H
A:Molecule type: nucleic acid
A:Residues: 1-16 <SL>
A:Notes: sequence extracted from NDBI backbone (NCBI:128349)
Query Match 25.0% Score 21; DB 2; Length 16;
Best Local Similarity 50.0% Prod. No. 4, 2e-03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy: 8 MKKQK 13
Db: 4 MKKSK 9

Search completed: January 28, 2003, 08:54:57
Job Time : 16 secs

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Db          3  K0289VA 10

RESULT 15
LPW_THETH  STANDARD;          PRT: 11 AA.
ID  LPW_THETH
DT  01-NOV-1988 (REL. 09, Created)
DT  01-NOV-1988 (REL. 09, Last sequence update)
DT  30-MAY-2000 (REL. 39, Last annotation update)
DE  10-residue leader peptide.
GN  TRPL
OS  Thermus thermophilus.
OC  Bacteria; Deinococcus group; Deinococci; Thermales;
OC  Thermaceae; Thermus
OC  NCBI_TaxId=274;
RP  SEQUENCE FROM N.A.
RC  STRAIN=HB8 / ATCC 27634;
RC  STRAIN=HB8 / ATCC 27634;
RA  Saito S., Nakada Y., Tanaka T.;
RA  "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT  HB8 type and trpD", J. Mol. Biol. 950:303-312(1988).
CC  1-1" FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC  OF TRYPTOPHAN.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the S.M.A.S Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by any bioinformatics institution, provided that the entry is not
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  for details).
CC  -----
CC  RML: X07744; CAA30565.1; -.
CC  -----
KW  Tryptophan biosynthesis; Leader peptide.
SO  SEQUENCE 11 AA: 1228 MW: 364825672DC5A7 CRC64;

Query Match      21.4%; Score 18; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy  2  LKVLV 7
Db          3  LKSLV 8

Search completed, January 28, 2003, 09:54:00
Job time : 12 secs

```



DT 01-MAY-1998 (TRENDEL). 08. Last annotation update)  
 GN C. (Fragment).  
 CC Escherichia coli.  
 CC Enterobacteriaceae; gamma subdivision: Enterobacteriaceae;  
 CC Escherichia.  
 OX NCBI\_TaxID=562;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9113957; PubMed=195589;  
 RA MEDLINE=9113957; PubMed=195589;  
 RT A family of regulators, genes associated with type II restriction-  
 modification systems. \*  
 RL J. Bacteriol. 173:1367-1375 (1991).  
 RL J. Bacteriol. 173:1367-1375 (1991).  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA: 1705 MW: 778626058IAF3B CRC64;  
 Query Match 32.1%; Score 27; DB 2; Length 14;  
 Best Local Similarity 45.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 LKRVIAKQKD 12  
 Db 1 LKRVIAKQKD 12  
 DB 1 LKRVIAKQKD 12  
 RESULT 3  
 ID 090DC7 PRELIMINARY: PRT: 15 AA.  
 DT 01-MAY-2000 (TRENDEL). 13. Created  
 DT 01-MAY-2000 (TRENDEL). 13. Last sequence update  
 DT 01-MAY-2000 (TRENDEL). 13. Last annotation update  
 DT 01-DEC-2001 (TRENDEL). 19. Last annotation update  
 CS Homo sapiens (human).  
 CC Buarayota. Metacoar. Chordata: Craniata: Vertebrata: Euteleostomi:  
 CC Buarayota. Metacoar. Chordata: Craniata: Vertebrata: Euteleostomi:  
 CC Buarayota. Metacoar. Chordata: Craniata: Vertebrata: Euteleostomi:  
 OX NCBI\_TaxID=9608;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9405921; PubMed=8241100;  
 RA Novotny W.P., Maffi T., Melia R.L., Miller P.G.;  
 RT A family of regulators, genes associated with type II restriction-  
 modification systems. \*  
 RL Atherosclerosis. Thromb. 13:1798-1805 (1993).  
 RL Atherosclerosis. Thromb. 13:1798-1805 (1993).  
 SQ SEQUENCE 15 AA: 1527 MW: C34869578474AC CRC64;  
 Query Match 31.0%; Score 26; DB 4; Length 15;  
 Best Local Similarity 81.3%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 KKKDKV 14  
 Db 9 KKKDKV 14  
 DB 9 KKKDKV 14  
 RESULT 4  
 ID 090DC7 PRELIMINARY: PRT: 15 AA.  
 DT 01-MAY-2000 (TRENDEL). 13. Created  
 DT 01-MAY-2000 (TRENDEL). 13. Last sequence update  
 DT 01-MAY-2000 (TRENDEL). 13. Last annotation update  
 DT 01-DEC-2001 (TRENDEL). 19. Last annotation update  
 CS Homo sapiens (human).  
 CC Buarayota. Metacoar. Chordata: Craniata: Vertebrata: Euteleostomi:  
 CC Buarayota. Metacoar. Chordata: Craniata: Vertebrata: Euteleostomi:  
 CC Buarayota. Metacoar. Chordata: Craniata: Vertebrata: Euteleostomi:  
 OX NCBI\_TaxID=9608;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9405921; PubMed=8241100;  
 RA Novotny W.P., Maffi T., Melia R.L., Miller P.G.;  
 RT A family of regulators, genes associated with type II restriction-  
 modification systems. \*  
 RL Atherosclerosis. Thromb. 13:1798-1805 (1993).  
 RL Atherosclerosis. Thromb. 13:1798-1805 (1993).  
 SQ SEQUENCE 15 AA: 1527 MW: C34869578474AC CRC64;  
 Query Match 31.0%; Score 26; DB 4; Length 15;  
 Best Local Similarity 81.3%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 9 KKKDKV 14  
 Db 9 KKKDKV 14  
 DB 9 KKKDKV 14  
 RESULT 5  
 ID 090DC7 PRELIMINARY: PRT: 13 AA.  
 DT 01-MAY-2000 (TRENDEL). 13. Created  
 DT 01-MAY-2000 (TRENDEL). 13. Last sequence update  
 DT 01-DEC-2001 (TRENDEL). 19. Last annotation update  
 DE Csa peptidase (Fragment).  
 OS Streptococcus pyogenes.  
 CC Bacteria: Firmicutes; Bacillus/Clostridium group: Lactobacillales;  
 CC Bacteria: Firmicutes; Bacillus/Clostridium group: Lactobacillales;  
 CC Bacteria: Firmicutes; Bacillus/Clostridium group: Lactobacillales;  
 OX NCBI\_TaxID=1314;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96298075; PubMed=9612622;  
 RA Sarge A., Naessens M., Bjork L.;  
 RT Virulence factors of Streptococcus pyogenes. \*;  
 RL Infect. Immun. 66:3449-3453 (1998).  
 RL Infect. Immun. 66:3449-3453 (1998).  
 DR MEROPS: S08-020-...  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA: 1603 MW: 5EADACCA6CE6723 CRC64;  
 Query Match 28.2%; Score 24.5; DB 2; Length 13;  
 Best Local Similarity 81.3%; Pred. No. 1.7e+03;  
 Matches 7; Conservative 1; Mismatches 0; Indels 3; Gaps 1;  
 Qy 8 KKKDKV 15  
 Db 3 KKKDKV 15  
 DB 3 KKKDKV 15  
 RESULT 6  
 ID 090DC7 PRELIMINARY: PRT: 13 AA.  
 DT 01-MAY-2000 (TRENDEL). 13. Created  
 DT 01-MAY-2000 (TRENDEL). 13. Last sequence update  
 DT 01-MAY-2000 (TRENDEL). 13. Last annotation update  
 DE 30S ribosomal protein S12 homolog (Fragment).  
 OS Mycobacterium bovis.  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;  
 OX NCBI\_TaxID=1765;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9400953; PubMed=8405418; Unpub. n.  
 RA Isolation and amino acid sequence of the 30S ribosomal protein S19  
 from Mycobacterium bovis BCG. \*;  
 RL J. Biol. Chem. 268:15115-15119 (1993).  
 RL J. Biol. Chem. 268:15115-15119 (1993).  
 SQ SEQUENCE 13 AA: 1603 MW: 78810A51B653234 CRC64;  
 Query Match 28.6%; Score 24; DB 2; Length 15;  
 DB 28.6%; Score 24; DB 2; Length 15;

RA Blase S.W., Wilson V., Watkins J.E., Oheroff N.;  
 RL J. Biol. Chem. 270:1911-1920 (1995).  
 DR SDD: S0005032; TOR2.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 15 AA: 2054 MW: 0A6A376EEEB8596 CRC64;  
 Query Match 29.8%; Score 25; DB 3; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 MKKDKV 16  
 Db 2 YKKDKV 16  
 DB 2 YKKDKV 16  
 RESULT 7  
 ID 090DC7 PRELIMINARY: PRT: 13 AA.  
 DT 01-MAY-2000 (TRENDEL). 13. Created  
 DT 01-MAY-2000 (TRENDEL). 13. Last sequence update  
 DT 01-DEC-2001 (TRENDEL). 19. Last annotation update  
 DE Csa peptidase (Fragment).  
 OS Streptococcus pyogenes.  
 CC Bacteria: Firmicutes; Bacillus/Clostridium group: Lactobacillales;  
 CC Bacteria: Firmicutes; Bacillus/Clostridium group: Lactobacillales;  
 CC Bacteria: Firmicutes; Bacillus/Clostridium group: Lactobacillales;  
 OX NCBI\_TaxID=1314;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96298075; PubMed=9612622;  
 RA Sarge A., Naessens M., Bjork L.;  
 RT Virulence factors of Streptococcus pyogenes. \*;  
 RL Infect. Immun. 66:3449-3453 (1998).  
 RL Infect. Immun. 66:3449-3453 (1998).  
 DR MEROPS: S08-020-...  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA: 1603 MW: 5EADACCA6CE6723 CRC64;  
 Query Match 28.2%; Score 24.5; DB 2; Length 13;  
 Best Local Similarity 81.3%; Pred. No. 1.7e+03;  
 Matches 7; Conservative 1; Mismatches 0; Indels 3; Gaps 1;  
 Qy 8 KKKDKV 15  
 Db 3 KKKDKV 15  
 DB 3 KKKDKV 15  
 RESULT 8  
 ID 090DC7 PRELIMINARY: PRT: 13 AA.  
 DT 01-MAY-2000 (TRENDEL). 13. Created  
 DT 01-MAY-2000 (TRENDEL). 13. Last sequence update  
 DT 01-MAY-2000 (TRENDEL). 13. Last annotation update  
 DE 30S ribosomal protein S12 homolog (Fragment).  
 OS Mycobacterium bovis.  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;  
 OX NCBI\_TaxID=1765;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9400953; PubMed=8405418; Unpub. n.  
 RA Isolation and amino acid sequence of the 30S ribosomal protein S19  
 from Mycobacterium bovis BCG. \*;  
 RL J. Biol. Chem. 268:15115-15119 (1993).  
 RL J. Biol. Chem. 268:15115-15119 (1993).  
 SQ SEQUENCE 13 AA: 1603 MW: 78810A51B653234 CRC64;  
 Query Match 28.6%; Score 24; DB 2; Length 15;



DE Similar to bni3 and sin recombinases of *Staphylococcus aureus*  
 OS (Fragment).  
 OS *Staphylococcus simulans*.  
 AC Bacillus/Clostridium group; Bacillales;  
 OC *Staphylococcus*.  
 OC NCHI\_TaxID=1286;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97260121; PubMed=9106216;  
 RA "Gamm G., Gutz P., Postaphin processing and characterization of the  
 PF lysoaphin immunity factor (Lif) of *Staphylococcus simulans* biovar  
 PF *staphylophilus*."; 351-1265(1997).  
 DR EMBL: U66893; AB037861.1.  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA: 1808 MW; 1044ABIEIEICFF CRC64;  
 Query Match Score 21; DB 2; Length 15;  
 Best Local Similarity 25.0%; Pred. No. 1e04; 4; Indels 0; Gaps 0;  
 Matches 3; Conservative 5; Mismatches 4;  
 Oy 3 KEVLMKKQKRV 14  
 Db 4 RQVYSIMDKV 15

RESULT 12  
 ID Q95886 PRELIMINARY; PRT: 15 AA.  
 AC Q95886  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Valine sensitive acetolactate synthase large subunit (EC 4.1.3.18)  
 DE (Fragment).  
 DE *Serratia marcescens*.  
 DE *Serratia*.  
 OC Serratia.  
 OC Serratia.  
 OC NCHI\_TaxID=615;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9328409; PubMed=4507653;  
 RA "Pudification and characterization of the valine sensitive  
 PF acetolactate synthase from *Serratia marcescens* ATCC 25419".  
 RA Biochim. biophys. Acta 1157:178-184(1993).  
 DR EMBL: AF041515.1; AF15 MW; C5314503AN565 CRC64;  
 SQ SEQUENCE 15 AA: 1615 MW; C5314503AN565 CRC64;  
 Query Match Score 24; DB 2; Length 15;  
 Best Local Similarity 25.0%; Pred. No. 1e04; 2; Indels 0; Gaps 0;  
 Matches 3; Conservative 1; Mismatches 2;  
 Oy 7 WKQKQD 12  
 Db 9 MARQLD 14

RESULT 13  
 ID Q96LJ0 PRELIMINARY; PRT: 15 AA.  
 AC Q96LJ0  
 DT 01-MAY-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)  
 DE Calpactin light chain-like protein (Fragment).  
 DE *Sus scrofa* (pig).  
 DE *Sus*.  
 OC Sus scrofa (pig).  
 OC Sus scrofa.  
 OC Sus scrofa.  
 OC NCHI\_TaxID=9923;  
 RP SEQUENCE FROM N.A.  
 RX Smith T.P.L., Fahrentkrug S.C., Rohrer G.A., Simmen F.A.,

Parced C.E. III, Keale J.W.;  
 \*Mapping of Expressed Sequence Tags from a porcine early embryonic  
 cDNA library, 1999, to the EMBL/GenBank/DBS databases.  
 DR EMBL: AF267116; AAC25933.1.  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA: 1925 MW; F9FF830F9921E CRC64;  
 Query Match Score 21; DB 6; Length 13;  
 Best Local Similarity 55.6%; Pred. No. 1e-04; 3; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 1;  
 Oy 5 VLVKKQKRV 13  
 Db 6 VLVKKQKRV 14

RESULT 14  
 ID Q9CBT2 PRELIMINARY; PRT: 16 AA.  
 AC Q9CBT2  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DE Mitochondrial cytochrome b (Cytb) (Fragment).  
 DE Mitochondrial cytochrome b (Cytb) (Fragment).  
 GN NFE3.  
 OS *Mus musculus* (Mouse).  
 OS *Mus musculus*.  
 OC Mus musculus (Mouse).  
 OC Mus musculus.  
 OC Mus musculus.  
 OC NCHI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=EMBRYO;  
 RX MEDLINE=31051660; PubMed=11171851;  
 RA Akirane T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Iwase M., Mishi K., Kiyosawa H., Kondo S., Yamana H.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Natsuo S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kishida H.,  
 RA Schirai I.W., Staubli P., Suzuki R., Tonita M., Wagner M., Washio T.,  
 RA Sakai K., Oikido T., Furuno M., Aono H., Balgarelli R., Barsh G.,  
 RA Blake J., Boerlein D., Bojunga N., Carlini P., de Bonaldo M.F.,  
 RA Gustiguchi S., Hill D., Hofmann M., Hume D.A., Kariye M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monteiro P.,  
 RA Suzuki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-P.,  
 RA Hsuah H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Hayashizaki Y.A., Tomoda K., Hasegawa Y., Kawaji H., Kortsch S.,  
 RX "Functional annotation of a full-length mouse cDNA collection".  
 RX Nucleic Acids Res. 29:100-103(2001).  
 DR EMBL: AF0404075; AAC21157.1.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA: 1891 MW; 0395FC9C0305363 CRC64;  
 Query Match Score 21; DB 11;  
 Best Local Similarity 25.0%; Pred. No. 1e-04; 2; Indels 0; Gaps 0;  
 Matches 3; Conservative 3; Mismatches 2;  
 Oy 2 IREYV 7  
 Db 8 LASEV 13

RESULT 15  
 ID Q9UWAD PRELIMINARY; PRT: 9 AA.  
 AC Q9UWAD  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

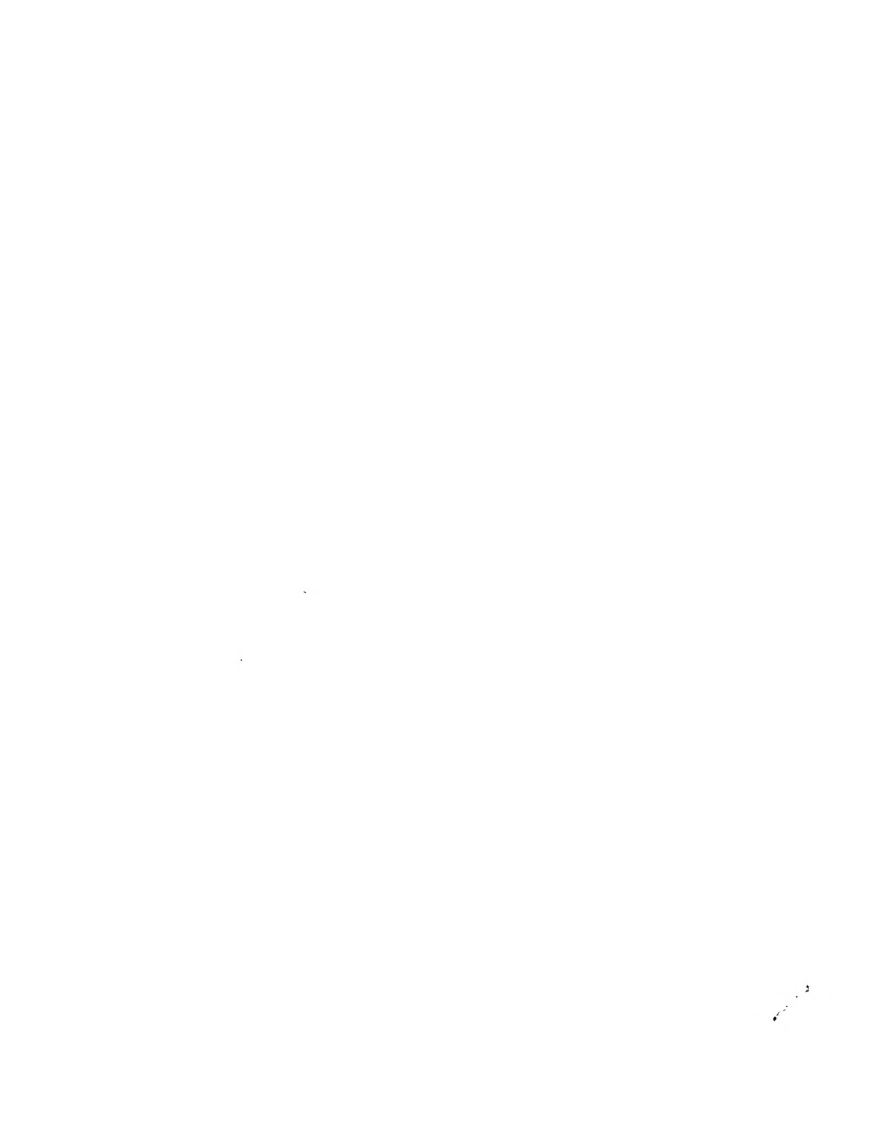


```

DT 01-MAY-2000 (TRENBLUel. 13. Last sequence update)
DN 01-MAY-2000 (TRENBLUel. 13. Last annotation update)
DR K17 Protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Hominidae; Homininae; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
EX REFERENCE FROM N.A.
EX MEDLINE=94061059; PubMed=7694728;
BA Spritz R.A., Holmes S.A., Berg S.Z., Nordlund J.J., Fukui K.;
BA "Resurrection of the human proco gene: a new member of the
BA proco gene family (proco-occase) is a frequent cause of human plebeidism."
BA Hum. Mol. Genet. 2:1459-1500(1993).
EL DBL, S57686; AAC13995.1; -.
DR DBL, S57686; AAC13995.1; -.
SO SEQUENCE 9 AA: 1182 MW; 0BC50403261B5AB CRC64;
Query Match 23.8%; Score 20; DB A; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 7 MKKQ 10
DD 11::
DD 5 MKRE 8

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Search completed: January 28, 2003, 09:54:36  
 Job time : 32 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: January 28, 2003, 08:42:09 Search time 34 Seconds  
(without alignments)  
(2,700 Million cell updates/sec)

Title: US-09-730-465-2\_COPY\_50\_65  
Sequence: 1 PLKEVLRKQKVALE 16  
Scoring table: RCGSW63  
Gap: 11.0, Gapext 0.5  
Searched: 908470 seqs, 13320620 residues  
Total number of hits satisfying chosen parameters: 255767  
Minimum DB seq length: 0  
Maximum DB seq length: 16  
Post-processing: Minimum Match 40  
Maximum Match 100  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the best hit being printed,  
and is derived by analysis of the local score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	42.9	16	23	AAE23846
2	36	42.9	16	23	AAE23847
3	36	42.9	16	23	AAE23848
4	35	42.9	16	23	AAE19852
5	35	41.7	15	16	AAE17348
6	34	40.5	10	21	AAE16583
7	34	40.5	10	21	AAE16583
8	34	40.5	15	23	AAE15893
9	32	36.1	14	22	AAE98523
10	32	36.1	16	15	AAE65027

11	31	36.9	8	23	AAU76075
12	31	36.9	9	23	AAU76074
13	31	36.9	11	22	AAU76076
14	31	36.9	11	22	AAU76110
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17	31	36.9	12	23	AAU76107
18	31	36.9	12	23	AAU76107
19	31	36.9	12	23	AAU76112
20	31	36.9	12	23	AAU76112
21	31	36.9	14	18	AAU24446
22	31	36.9	14	22	AAU98520
23	31	36.9	14	22	AAU98520
24	31	36.9	16	21	AAU52664
25	30	35.7	8	18	AAU44604
26	30	35.7	8	20	AAU55501
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29	30	35.7	9	18	AAU44562
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31	30	35.7	9	22	AAU55501
32	30	35.7	14	14	AAU31887
33	30	35.7	14	14	AAU31887
34	30	35.7	16	30	AAU42318
35	29	34.5	13	22	AAU03136
36	29	34.5	15	22	AAU55502
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38	29	34.5	15	16	AAU81042
39	29	34.5	15	16	AAU87770
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43	29	34.5	15	18	AAU31657
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## ALIGNMENTS

RESULT 1  
AAE23846  
17 AAU76846 standard; peptide: 16 aa.  
XX AAE23846;  
10-SEP-2002 (first entry)  
XX Human zslg33-gamma peptide #2.  
XX Human zslg33-gamma peptide #2.  
XX Human zslg33-gamma peptide; gastric contractility; nutrient uptake;  
XX growth hormone; digestive enzyme; restorative therapy; gene therapy;  
XX protein therapy; gastrointestinal; endocrine; antibiotic.  
XX Homo sapiens.  
XX US02002055156-A1.  
XX 09-MAY-2002.

XX 10-MAY-2001: 2001US-085323.  
XX 11-MAY-2000: 2000US-203300P.  
XX (JASP)/ JASPER S. R.  
XX (SHEP)/ SHEPARD P. O.  
XX (BISH)/ BISHOP P. D.  
XX Jaspers SR, Sheppard PO, Delaher TH, Bishop PD;  
XX WPI: 2002-443750/47.



XX Claim 3b; Page 85; 89pp: English.

XX The invention relates to zsig33-like peptides (z33LP) including

XX zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and such

XX zsig33-epsilon peptides and nucleic acid molecules encoding such

XX peptides, and methods for using the same, for example, in

XX boosting immunity to infectious diseases, treating immunocompromised

XX patients such as human immunodeficiency virus (HIV) patients, in

XX the treatment of cancer, and in the treatment of bacterial, viral, and

XX fungal infections. Peptides of the invention are used to identify and

XX isolate receptors involved in growth regulation in the liver, blood for

XX vascular formation and other developmental processes. They are useful for

XX growth and/or differentiation of tumour cells, as additives to anti-

XX tumour growth and/or differentiation of tumour cells, as additives to anti-

XX stimulate glucose-induced insulin release. They are also useful as

XX research reagents for the expansion, differentiation, growth factor and

XX with gastrointestinal system, brain and central nervous system. These

XX molecules are useful for treating dysfunction associated with contractile

XX gastrointestinal and growth related diseases. z33LP peptides, nucleic

XX acids and/or antibodies are useful for treating disorders associated

XX with gastrointestinal contractility, secretion of digestive enzymes,

XX gastrointestinal motility, recruitment of digestive enzymes, inflammation

XX and regulation of nutrient absorption. Sequences of the invention are

XX useful in gene therapy. The present sequence is human zsig33-gamma

XX peptide.

XX Sequence 16 AA;

Query Match 42.9%; Score 36; DB 23; Length 16;

Best Local Similarity 33.3%; Pred. No. 6;

Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKRVKAKKQDKVAV 16

DB 2 LQDIMEAKDAPD 16

RESULT 4

AD AAEL5892 standard; peptide; 16 AA.

AC AAEL5892;

XX 26-MAR-2002 (first entry)

XX Human zsig33-gamma peptide #3.

DE Human zsig33-gamma peptide #3.

KN Infection; human immunodeficiency virus; vaccine; antihypoglycemic;

KN inflammation; gene therapy; growth regulation; blood vessel formation.

KN HIV; zsig33-gamma peptide.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site /note= "C-terminal amide"

XX W0200107933-A2.

XX 22-NOV-2001.

XX 10-MAY-2001; 2001WO-0815091.

XX 11-MAY-2000; 2000US-0569271.

PA (ZYMO ) ZYMOGENETICS INC.

XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

DR WPI; 2002-082982/11.

DR N-FDB; AM2574.

XX New polypeptides, useful for modulating gastric contractility, nutrient

XX uptake, pancreatic secretion of hormones, digestive enzymes and

XX gastrointestinal and growth related diseases. Comprises

XX zsig33-like peptides -

XX Claim 5c; Page 85; 89pp: English.

XX The invention relates to zsig33-like peptides (z33LP) including

XX zsig33-linker, zsig33-beta, zsig33-gamma, zsig33-delta and such

XX zsig33-epsilon peptides. z33LP peptides activate the immune system

XX in boosting immunity to infectious diseases, treating immunocompromised

XX patients such as human immunodeficiency virus (HIV) patients, in

XX the treatment of cancer, and in the treatment of bacterial, viral, protozoal and

XX fungal infections. Peptides of the invention are used to identify and

XX isolate receptors involved in growth regulation in the liver, blood for

XX vascular formation and other developmental processes. They are useful for

XX growth and/or differentiation of tumour cells, as additives to anti-

XX tumour growth and/or differentiation of tumour cells, as additives to anti-

XX stimulate glucose-induced insulin release. They are also useful as

XX research reagents for the expansion, differentiation, growth factor and

XX with gastrointestinal system, brain and central nervous system. These

XX molecules are useful for treating dysfunction associated with contractile

XX gastrointestinal and growth related diseases. z33LP peptides, nucleic

XX acids and/or antibodies are useful for treating disorders associated

XX with gastrointestinal contractility, secretion of digestive enzymes,

XX gastrointestinal motility, recruitment of digestive enzymes, inflammation

XX and regulation of nutrient absorption. Sequences of the invention are

XX useful in gene therapy. The present sequence is human zsig33-gamma

XX peptide.

XX Sequence 16 AA;

Query Match 42.9%; Score 36; DB 23; Length 16;

Best Local Similarity 33.3%; Pred. No. 76;

Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKRVKAKKQDKVAV 16

DB 2 LQDIMEAKDAPD 16

RESULT 5

AD AAEL7348 standard; peptide; 15 AA.

AC AAEL7348;

XX 04-DEC-1995 (first entry)

XX Fragment of P.sergenti, 33 kDa protein.

XX bovine small proplasma protozoa; 33 kDa protein; vaccine;

XX immunogen.

XX Theileria sergenti.

XX AU9470373-A.

XX 09-MAR-1995.





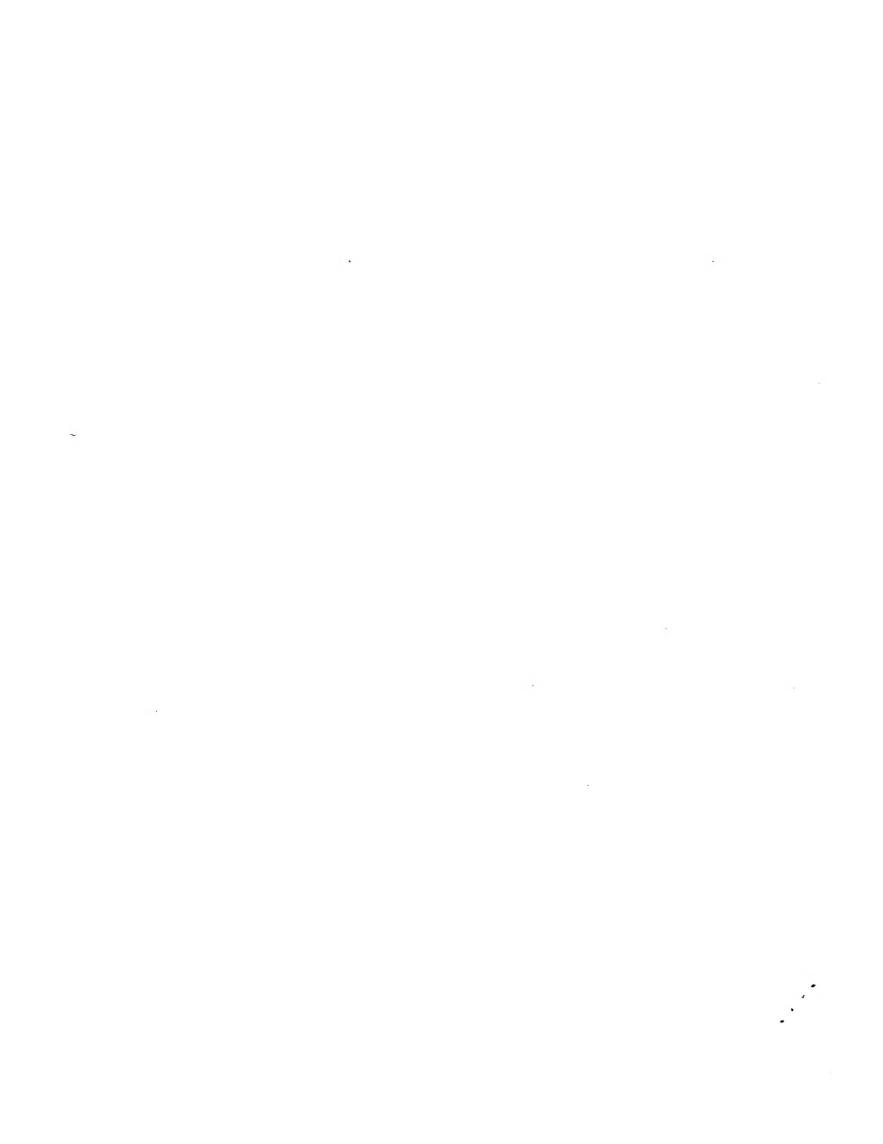












GenCore version 5.1.3

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OK protein - protein search, using sw model

Run on: January 28, 2003, 08:54:40 ; Search time 11 Seconds

Without alignments

29,331 Million cell updates/sec

Title: us-09-730-465-2\_COPY\_50\_65

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Searched:

122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 31115

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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 and is derived by analysis of the total score distribution.

## SUMMARIES

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7	26	31.0	10	10	US-09-984-056-45
8	26	31.0	10	10	US-09-984-056-45
9	26	31.0	11	10	US-09-791-398-402
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12	26	31.0	15	10	US-09-766-396-23
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44	25	29.8	15	10	US-09-765-527-18
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46	25	29.8	15	10	US-09-765-527-20

## ALIGNMENTS

RESULTS 1  
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 : Patent No. US20020055156A1  
 : GENERAL INFORMATION: STEPHEN  
 : APPLICANT: SHEPPARD, PAUL  
 : APPLICANT: DESHNER, THERESA  
 : TITLE OF INVENTION: Zsig33-like Peptides  
 : FILE REFERENCE: 00-30  
 : PARENT PUBLICATION NUMBER: US/09-053,253  
 : CURRENT FILING DATE: 2001-05-10  
 : PRIOR APPLICATION NUMBER: 60/203,300  
 : PRIOR FILING DATE: 2000-05-11  
 : SOFTWARE: FASTSEQ FOR Windows Version 3.0  
 : SEQ ID NO 15  
 : TYPE: PPT  
 : ORGANISM: Homo sapiens  
 : US-09-853-253-15

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 Matches 5; Conservative 7; Alignments 3; Gaps 0;

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DB	2	LEKVIYLRKQKQYAE	16

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 : Sequence 16 Application US/09851253  
 : Patent No. US20020055156A1  
 : GENERAL INFORMATION: STEPHEN  
 : APPLICANT: JASPERS, STEPHEN  
 : APPLICANT: DESHNER, THERESA  
 : TITLE OF INVENTION: Zsig33-like Peptides



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1  APPLICANT: Better, Marc D.
2  TITLE OF INVENTION: Methods for Recombinant Microbial Production of
3  Peptide Sequences of Bacterial Proteins and BPI-derived Peptides
4  NUMBER OF SEQUENCES: 26
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Ciba, Ltd., P.O. Box 561, CH-4002, Basel, Switzerland
7  ADDRESSEE: Ciba, Ltd., P.O. Box 561, CH-4002, Basel, Switzerland
8  CITY: Chicago
9  STATE: Illinois
10  COUNTRY: United States of America
11  FILING DATE: 18-Jan-2001
12  PUBLICATION DATE: 05/09/2001
13  APPLICATION NUMBER: 08/421,003
14  INVENTOR: Marc D. Better
15  NAME: Robert B. Townsend
16  REGISTRATION NUMBER: 25,447
17  REFERENCE/DOCKET NUMBER: 27129/31199
18  TELEPHONE: 312/474-6300
19  TELEFAX: 312/474-0448
20  INFORMATION FOR SEQ ID NO: 101:
21  SEQUENCE CHARACTERISTICS:
22  LENGTH: 15 amino acids
23  TYPE: Peptide
24  TOPOLOGY: Linear
25  MOLECULE TYPE: Peptide
26  FRAGMENT: 1-15
27  NAME/KEY: misc-feature
28  OTHER INFORMATION: "MP-120"
29  NAME/KEY: Modified-site
30  LOCATION: C-Terminal
31  OTHER INFORMATION: /label: Mutation
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33  SEQUENCE DESCRIPTION: SEQ ID NO: 101:
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39  QY 7 MKKQKDV 14
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42  RESULT 5
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44  Sequence 74, Application US/09071838
45  BEST LOCAL SIMILARITY 62.3% Pred. No. 88;
46  GENERAL INFORMATION:
47  APPLICANT: Fischer, Robert L.
48  APPLICANT: Ohad, Nir
49  APPLICANT: Yehoshua, Yehoshua
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99  APPLICANT: Yehoshua, Yehoshua
100 APPLICANT: Yehoshua, Yehoshua

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1  STREET: Two Embarcadero Center, Eighth Floor
2  CITY: San Francisco
3  STATE: California
4  COUNTRY: USA
5  ZIP: 94111-3834
6  COMPUTER READABLE FORM: disk
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8  COMPUTER: IBM PC compatible
9  CURRENT APPLICATION DATA: 1.0, Version #1.30
10  APPLICATION NUMBER: US/09/071,838
11  INVENTOR: Marc D. Better
12  NAME: Robert B. Townsend
13  REGISTRATION NUMBER: 25,447
14  REFERENCE/DOCKET NUMBER: 021070-08610005
15  TELEPHONE: 415/576-6300
16  TELEFAX: 415/576-6300
17  INFORMATION FOR SEQ ID NO: 74:
18  SEQUENCE CHARACTERISTICS:
19  LENGTH: 9 amino acids
20  TYPE: amino acid
21  TOPOLOGY: linear
22  FRAGMENT: 1-9
23  NAME/KEY: misc-peptide
24  OTHER INFORMATION: "MP-120"
25  NAME/KEY: Modified-site
26  LOCATION: C-Terminal
27  OTHER INFORMATION: /label: Mutation
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33  Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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36  DB 6 LKQKQKDV 13
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41  BEST LOCAL SIMILARITY 50.0% Pred. No. 1er005;
42  GENERAL INFORMATION:
43  APPLICANT: Fischer, Robert L.
44  APPLICANT: Ohad, Nir
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48  APPLICANT: Yehoshua, Yehoshua
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QY 8 LKQKQKDV 13
DB 8 LKQKQKDV 13

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QY 8 LKQKQKDV 13
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1 COUNTRY: US
2 ZIP: 92037
3 COMPUTER: IBM compatible
4 MEDIUM TYPE: Floppy disk
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6 CURRENT APPLICATION DATA:
7   CURRENT APPLICATION DATA: PC-DOS/MS-DOS, Version #1.25
8   APPLICATION NUMBER: US/10/062.375
9   CLASSIFICATION: <unknown>
10 PRIOR APPLICATION DATA:
11   APPLICATION NUMBER: US/08/657.389
12   FILING DATE: <unknown>
13 ATTORNEY/AGENT INFORMATION:
14   NAME: Schmonsees, William
15   REFERENCE/DOCKET NUMBER: 22908-0002
16 TELECOMMUNICATION INFORMATION:
17   TELEPHONE: (415) 324-0638
18   TELEFAX: (415) 324-0638
19 INFORMATION FOR SEQ ID NO: 8:
20   SEQ ID NO: 8
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27 Db 1 PCNFWK 8
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31 Sequence 23, Application US/0766396
32 Patent No. US20020135641
33 GENERAL INFORMATION:
34   APPLICANT: Sutcliffe, Gregor J.
35   ORGANISM: Human
36   TITLE OF INVENTION: NEUROPEPTIDES,
37   HENRIKSEN, STEVEN J.
38 CORRESPONDENCE ADDRESS:
39   ADDRESS: 10658 JEFFERSON AVE
40   CITY: La Jolla
41   STATE: California
42   COUNTRY: US
43 ZIP: 92037
44 COMPUTER-READABLE FORM:
45   OPERATING SYSTEM: IBM PC compatible
46   CURRENT APPLICATION DATA:
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49     CLASSIFICATION: <unknown>
50 PRIOR APPLICATION DATA:
51   APPLICATION NUMBER: 08/657.389
52   ATTORNEY/AGENT INFORMATION:
53     NAME: Schmonsees, William
54
55 REFERENCE/DOCKET NUMBER: 22908-0002
56 TELEPHONE: (415) 324-0638
57 TELEFAX: (415) 324-0638
58 INFORMATION FOR SEQ ID NO: 10:
59   SEQ ID NO: 10
60   SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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70 Patent No. US20020064770A1
71 GENERAL INFORMATION:
72   APPLICANT: See, Raymond
73   ORGANISM: Human
74   TITLE OF INVENTION: Peptide Binding Compounds and Methods for Identifying Binding Compound
75   APPLICANT: Sutcliffe, Gregor J.
76   ORGANISM: Human
77   FILE REFERENCE: CNS-005
78   CURRENT APPLICATION NUMBER: US/09/813,653
79   PRIOR APPLICATION NUMBER: US 60/190,946
80   PRIOR FILING DATE: 2000-03-21
81   PRIOR FILING DATE: 2000-03-21
82   PRIOR FILING DATE: 2000-03-21
83   PRIOR FILING DATE: 2000-03-21
84   SOFTWARE: Patent version 3.0
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88   ORGANISM: Artificial sequence
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99 RESULT 14
100 US-09-813-653-23
101 Sequence 23, Application US/10062375
102 Patent No. US200201300041
103 GENERAL INFORMATION:
104   APPLICANT: Sutcliffe, Gregor J.
105   ORGANISM: Human
106   TITLE OF INVENTION: NEUROPEPTIDES,
107   SIGNAS, GEORGE R.
108   DE LECHE, LOUIS
109 COMPOSITIONS AND METHODS

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1 NUMBER OF SOURCES: 26  
 2 CORRESPONDENCE ADDRESS:  
 3 ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
 4 10550 LA JOLLA VILLAGE RD. US200/7013300Health Torrey Pines Road, TPC-8  
 5 STATE: La Jolla  
 6 COUNTRY: US  
 7 COUNTY: 078  
 8 COMPUTER READABLE FORM:  
 9 MEDIUM TYPE: Floppy disk  
 10 OPERATING SYSTEM: PC-DOS/MS-DOS  
 11 SOFTWARE: PatentIn Release #1.0. Version #1.25  
 12 CURRENT APPLICATION NUMBER: US/10/062,375  
 13 FILING DATE: 30-Jan-2002  
 14 CLASSIFICATION: <unknown>  
 15 PRIOR APPLICATION NUMBER: US/08/857,389  
 16 FILING DATE: <unknown>  
 17 ATTORNEY: Schenck, Smith & Peltz, LLP  
 18 NAME: Schenck, William  
 19 REGISTRATION NUMBER: 31,786  
 20 TELECOMMUNICATION INFORMATION:  
 21 TELEPHONE: (415) 324-7041  
 22 TELEFAX: (415) 324-0638  
 23 INFORMATION CATEGORIES:  
 24 SEQUENCE CHARACTERISTICS:  
 25 LENGTH: 15 amino acids  
 26 TOPOLOGY: Linear  
 27 MOLECULE TYPE: Protein  
 28 RECOMBINATION: Chemical  
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4	30	35.7	8	US-08-621-259A-105	Sequence 105, Appl 1
5	30	35.7	8	US-08-621-259A-105	Sequence 205, Appl 1
6	30	35.7	9	US-08-621-259A-163	Sequence 163, Appl 1
7	30	35.7	14	US-07-907-569-116	Sequence 116, Appl 1
8	30	35.7	14	US-07-907-569-116	Sequence 117, Appl 1
9	30	35.7	16	US-08-485-437-111	Sequence 111, Appl 1
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11	30	35.7	16	US-08-337-0552-111	Sequence 111, Appl 1
12	29	34.5	15	US-08-311-611A-116	Sequence 116, Appl 1
13	29	34.5	15	US-08-372-783-116	Sequence 116, Appl 1
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16	29	34.5	15	US-08-621-603-101	Sequence 101, Appl 1
17	29	34.5	15	US-08-621-603-101	Sequence 102, Appl 1
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28 27 5 32 7 12 2 US-08-659-984A-8  
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## ALIGNMENTS

5185441-12  
Patent No. 5185441  
INVENTOR: BARBARA P. HESTONS, CATHERINE  
TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA  
MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCTE  
FOURMOTOMY-INDUCED T-CELLS  
NUMBER OF SEQUENCES: 41  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/237,309  
FILING DATE: 26 AUG 1998  
SEQ ID NO:12:  
LENGTH: 7  
5185441-12

Query Match Similarity 50.0%; Score 42; DB 6; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

09 7 MKKQK 13

DB 1 MKKQK 7

RESULT 2  
US-09-050-411-5  
Sequence 5, Application US/99050811  
Patent No. 5137700  
GENERAL INFORMATION:  
APPLICANT: NICE, Kevin G.  
INVENTOR: NICE, Kevin G.  
TITLE OF INVENTOR: Peptides for Gene Delivery  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:  
ADDRESS: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
COMPUTER: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: 9/050.811  
FILING DATE: 26 MAR 1998  
CLASSIFICATION: 51A  
ATTORNEY/AGENT INFORMATION:

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1 NAME: Carroll, Peter G.
2 REGISTRATION NUMBER: 32,837
3 REFERENCE/DOCKET NUMBER: UN-03314
4 TELEPHONE: 415/705-8410
5 TELEFAX: 415/397-8338
6 INFORMATION FOR SEQ ID NO: 5:
7 SEQUENCE DESCRIPTION:
8 LENGTH: 10 amino acids
9 TYPE: amino acid
10 STRANDEDNESS: not relevant
11 TOPOLOGY: linear
12 MOLECULE TYPE: protein
13 FEATURE:
14 NAME/KEY: Binding-site
15 LOCATION: 1
16 OTHER INFORMATION: Note- "The residue at this
17 position is bound to an Alkaloid by a Sulfide."
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19 US-09-050-811-5
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25 DB 2 WKKKKK 8
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27 RESULT 3
28 US-09-0311-6
29 Sequence 6: Application US/09050811
30 Patent No. 6387700
31 GENERAL INFORMATION:
32 APPLICANT: Kevin G.
33 APPLICANT: Redive, Maupreet S.
34 TITLE OF INVENTION: Peptides for Gene Delivery
35 CORRESPONDENCE ADDRESS:
36 ADDRESSEE: MIDLIN & CARROLL, LLP
37 STREET: 220 Montgomery Street, Suite 2200
38 CITY: San Francisco
39 STATE: CA
40 COUNTRY: USA
41 ZIP: 94104
42 COMPUTER READABLE FORM:
43 MEDIUM TYPE: Floppy disk
44 OPERATING SYSTEM: PC-DOS/MS-DOS
45 SOFTWARE: Patentin Release #1.0 Version #1.30
46 APPLICATION NUMBER: US/09/050-811
47 CLASSIFICATION: 514
48 ATTORNEY/AGENT INFORMATION:
49 REFERENCE/DOCKET NUMBER: 32,837
50 REGISTRATION NUMBER: UN-03314
51 ADDRESSEE: MIDLIN & CARROLL, LLP
52 STREET: 220 Montgomery Street, Suite 2200
53 CITY: San Francisco
54 STATE: CA
55 COUNTRY: USA
56 ZIP: 94104
57 COMPUTER READABLE FORM:
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61 APPLICATION NUMBER: US/09/050-811
62 CLASSIFICATION: 514
63 FILING DATE: 30-MAR-1998
64 REGISTRATION NUMBER: 32,837
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Carroll, Peter G.
67 REGISTRATION NUMBER: UN-03314
68 TELEPHONE: 415/705-8410
69 INFORMATION FOR SEQ ID NO: 6:
70 SEQUENCE CHARACTERISTICS:
71 LENGTH: 15 amino acids
72 TYPE: amino acid
73 STRANDEDNESS: not relevant
74 TOPOLOGY: linear
75 MOLECULE TYPE: protein
76 FEATURE:
77 NAME/KEY: Binding-site
78 LOCATION:
79 OTHER INFORMATION: Note- "The residue at this
80 position is bound to an Alkaloid by a Sulfide."

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1 US-09-050-811-6
2 Query Match 36.9% Score 31; DB 4; Length 15;
3 Best Local Similarity 71.4% Pred. No. 951
4 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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6 QY 7 WKKKOK 13
7 DB 2 WKKKKK 8
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9 RESULT 4
10 US-09-050-811-11
11 Sequence 11: Application US/09050811
12 Patent No. 6387700
13 GENERAL INFORMATION:
14 APPLICANT: Rice, Kevin G.
15 APPLICANT: Redive, Maupreet S.
16 TITLE OF INVENTION: Peptides for Gene Delivery
17 CORRESPONDENCE ADDRESS:
18 ADDRESSEE: MIDLIN & CARROLL, LLP
19 STREET: 220 Montgomery Street, Suite 2200
20 CITY: San Francisco
21 STATE: CA
22 COUNTRY: USA
23 ZIP: 94104
24 COMPUTER READABLE FORM:
25 MEDIUM TYPE: Floppy disk
26 OPERATING SYSTEM: PC-DOS/MS-DOS
27 SOFTWARE: Patentin Release #1.0 Version #1.30
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29 CLASSIFICATION: 514
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32 REGISTRATION NUMBER: UN-03314
33 ADDRESSEE: MIDLIN & CARROLL, LLP
34 STREET: 220 Montgomery Street, Suite 2200
35 CITY: San Francisco
36 STATE: CA
37 COUNTRY: USA
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41 OPERATING SYSTEM: PC-DOS/MS-DOS
42 SOFTWARE: Patentin Release #1.0 Version #1.30
43 APPLICATION NUMBER: US/09/050-811
44 CLASSIFICATION: 514
45 ATTORNEY/AGENT INFORMATION:
46 REFERENCE/DOCKET NUMBER: 32,837
47 REGISTRATION NUMBER: UN-03314
48 ADDRESSEE: MIDLIN & CARROLL, LLP
49 STREET: 220 Montgomery Street, Suite 2200
50 CITY: San Francisco
51 STATE: CA
52 COUNTRY: USA
53 TELEPHONE: 415/705-8410
54 TELEFAX: 415/397-8338
55 INFORMATION FOR SEQ ID NO: 11:
56 SEQUENCE CHARACTERISTICS:
57 LENGTH: 15 amino acids
58 TYPE: amino acid
59 STRANDEDNESS: not relevant
60 TOPOLOGY: linear
61 MOLECULE TYPE: protein
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63 US-09-050-811-11
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65 Best Local Similarity 71.4% Pred. No. 951
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69 DB 2 WKKKKK 8
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71 RESULT 5
72 US-08-621-259A-205
73 Sequence 205: Application US/08621259A
74 Patent No. 6564400
75 GENERAL INFORMATION:
76 APPLICANT: Little II, Roger G.
77 APPLICANT: Fadem, Mitchell B.
78 TITLE OF INVENTION: Anti-Fungal Peptides
79 CORRESPONDENCE ADDRESS:
80 ADDRESSEE: McAndrews, Heid & Malloy, Ltd.

```

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1 STREET: 500 West Madison Street
2 CITY: Chicago
3 COUNTRY: Illinois
4 COUNTY: United States of America
5 ZIP: 60661
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7 COMPUTER READABLE FORM: disk
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9 COMPUTER: IBM PC compatible
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11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 RELEASE: Patent Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 PRIOR APPLICATION DATA:
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27 FEATURE:
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29     LOCATION: 1-8
30     OTHER INFORMATION: /note= "The C-Terminus is Amidated."
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1 APPLICANT: Lambert, Jr., Lewis H.  
 2 TITLE OF INVENTION: Increasing Gram-Negative Bacterial  
 3 TITLE OF INVENTION: Infection by Administration of  
 4 TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
 5 TITLE OF INVENTION: 227  
 6 CORRESPONDENCE ADDRESS:  
 7 ADDRESSEE: Marshall, O'Toole, Gerstein, Mursay & Borun  
 8 CITY: Chicago  
 9 STATE: Illinois  
 10 COUNTRY: USA  
 11 ZIP: 60606-6402  
 12  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: Floppy disk  
 15 MEDIUM TYPE: 5 1/4 inch  
 16 OPERATING SYSTEM: PC-DOS/MS-DOS  
 17 SOFTWARE: Patent Release #1.0, Version #1.25  
 18 COUNTRY OF ORIGIN: USA  
 19 APPLICATION NUMBER: US/09/311,611A  
 20  
 21 FILING DATE: 08/27/3,401  
 22 APPLICATION NUMBER: 08/273,401  
 23 PRIORITY DATA: 08/27/3,401  
 24 FILING DATE: 11-JUL-1994  
 25 PRIORITY DATA: 08/25,651  
 26 FILING DATE: 22-SEP-1993  
 27 PRIORITY DATA: 08/25,651  
 28 ATTORNEY/AGENT INFORMATION:  
 29 NAME: Marshall, O'Toole, Gerstein, Mursay & Borun  
 30 REGISTRATION NUMBER: 31,879  
 31 REFERENCE/DOCKET NUMBER: 32251  
 32 TELEPHONE: 312/474-6300  
 33 TELEFAX: 312/474-0448  
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 35 INFORMATION FOR SEQ ID NO: 116:  
 36 SEQUENCE CHARACTERISTICS:  
 37 TYPE: amino acid  
 38 TOPOLOGY: linear  
 39 MOLECULE TYPE: peptide  
 40 NAME/KEY: misc\_feature  
 41 OTHER INFORMATION: "BPT.120"  
 42 US-08-311-611A-116

Query Match 34.5%; Score 39; DB 1; Length 15;  
 Match 5; Conservative 1; Mismatches 2; Indels 0;  
 Gaps 0;

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Db 7 MAAKKRL 14

RESULT 13

US-08-372-781-116  
 Patent No. 5578572  
 GENERAL INFORMATION:  
 APPLICANT: Marshall, O'Toole, Gerstein, Mursay & Borun  
 APPLICANT: Lambert, Lewis H.  
 APPLICANT: Little, Roger G.  
 TITLE OF INVENTION: Increasing Gram-Negative Bacterial Methods and  
 TITLE OF INVENTION: Malt-048  
 NUMBER OF SEQUENCES: 237  
 CORRESPONDENCE ADDRESS:  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606-6402

1 COMPUTER READABLE FORM:  
 2 MEDIUM TYPE: Floppy disk  
 3 MEDIUM TYPE: 5 1/4 inch  
 4 OPERATING SYSTEM: PC-DOS/MS-DOS  
 5 SOFTWARE: Patent Release #1.0, Version #1.25  
 6 COUNTRY OF ORIGIN: USA  
 7 APPLICATION NUMBER: US/08/372,783  
 8  
 9 FILING DATE: 08/27/3,540  
 10 APPLICATION NUMBER: 08/273,540  
 11 PRIORITY DATA: 08/27/3,540  
 12 FILING DATE: 11-JUL-1994  
 13 PRIORITY DATA: 08/209,762  
 14 FILING DATE: 11-MAR-1994  
 15 PRIORITY DATA: 08/209,762  
 16 ATTORNEY/AGENT INFORMATION:  
 17 NAME: Marshall, O'Toole, Gerstein, Mursay & Borun  
 18 REGISTRATION NUMBER: 31,547  
 19 REFERENCE/DOCKET NUMBER: 32739/33415  
 20 TELEPHONE: 312/474-6300  
 21 TELEFAX: 312/474-0448  
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 23 INFORMATION FOR SEQ ID NO: 116:  
 24 SEQUENCE CHARACTERISTICS:  
 25 TYPE: amino acid  
 26 TOPOLOGY: linear  
 27 MOLECULE TYPE: peptide  
 28 NAME/KEY: misc\_feature  
 29 OTHER INFORMATION: "MMP.120"  
 30 US-08-372-783-116

Query Match 34.5%; Score 39; DB 1; Length 15;  
 Match 5; Conservative 1; Mismatches 2; Indels 0;  
 Gaps 0;

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Db 7 MAAKKRL 14

RESULT 14

US-08-372-105-116  
 Patent No. 5627153  
 GENERAL INFORMATION:  
 APPLICANT: Marshall, O'Toole, Gerstein, Mursay & Borun  
 APPLICANT: Lambert, Lewis H.  
 APPLICANT: Little, Roger G.  
 TITLE OF INVENTION: Increasing Gram-Negative Bacterial Methods and  
 TITLE OF INVENTION: Malt-048  
 NUMBER OF SEQUENCES: 227  
 CORRESPONDENCE ADDRESS:  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 MEDIUM TYPE: 5 1/4 inch  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 COUNTRY OF ORIGIN: USA  
 APPLICATION NUMBER: US/08/372,105  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/273,540



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2 FILING DATE: 11-JUL-1994
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 08/209,762
5 FILING DATE: 11-MAY-1994
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: 08/283,222
8 FILING DATE: 08-SEP-1994
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Rio-Laures, Li-Hsien
11 REFERENCE/DOCKET NUMBER: 27139/22415
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 312-715-1234
14 TELEFAX: 312-715-1234
15 INFORMATION FOR SEQ ID NO: 116:
16 LENGTH: 15 amino acids
17 TYPE: amino acid
18 MOLECULE TYPE: peptide
19 FEATURE:
20 NAME/KEY: misc-feature
21 OTHER INFORMATION: "BPI-120"
22 US-08-372-105-116
23
24 Query Match 34.5% Score 29; Db 1; Length 15;
25 Best Local Similarity 62.5% Pred. No. 1.9e+02;
26 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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29 Db 7 MKAKKKL 14
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33 Search completed: January 28, 2003, 08:55:39
34 Job time : 36 secs
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GenCode version 5.1.3

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OM protein - protein search, using sw model

Run on: January 28, 2003, 08:58:30 ; Search time 55 Seconds  
 (without alignments)  
 105,022 Million cell updates/sec

Title: us-09-730-465-2\_COPY\_20\_80

Sequence: 1 LKFGTSCSQQLGVYV.....DKVALESEFATFSFNR 61

Scoring table:

BLOSUM62

Gap-P 10.0 , Gapext 0.5

Searched:

283224 seqs, 9513422 residues

Total number of hits satisfying chosen parameters: 16420

Minimum DB seq length: 0

Maximum DB seq length: 61

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1: p1r3\*

2: p1r2\*

3: p1r1\*

4: p1r0\*

SUMMARY

Pred. No. is the number of results predicted by chance to have a

score of 16.42 or higher. The results are sorted by predicted

score and is derived by analysis of the total score distribution.

## SUMMARY

Result No.	Score	Match	Length	DB ID	Description
1	47	14	4	19	lactase-phlorizin
2	44	12	6	2	cytochrome P450 (C
3	42	12	6	2	conserved hypotet
4	42	12	8	60	small hydrophobic
5	41	12	7	2	small hydrophobic
6	41	12	7	2	small hydrophobic
7	41	12	5	2	small hydrophobic
8	41	12	5	2	small hydrophobic
9	40	12	5	2	small hydrophobic
10	40	12	5	2	small hydrophobic
11	39	12	5	2	small hydrophobic
12	39	12	5	2	small hydrophobic
13	39	12	5	2	small hydrophobic
14	39	12	5	2	small hydrophobic
15	39	12	5	2	small hydrophobic
16	39	12	5	2	small hydrophobic
17	39	12	5	2	small hydrophobic
18	39	12	5	2	small hydrophobic
19	39	12	5	2	small hydrophobic
20	39	12	5	2	small hydrophobic
21	39	12	5	2	small hydrophobic
22	39	12	5	2	small hydrophobic
23	39	12	5	2	small hydrophobic
24	39	12	5	2	small hydrophobic
25	39	12	5	2	small hydrophobic
26	39	12	5	2	small hydrophobic
27	39	12	5	2	small hydrophobic
28	39	12	5	2	small hydrophobic
29	39	12	5	2	small hydrophobic

30	37	11	3	49	2	D70228	hypothetical prote
31	37	11	3	55	2	D15680	sex-determining pr
32	37	11	3	55	2	D15680	sex-determining pr
33	36	11	2	39	2	D74393	hypothetical prote
34	36	11	2	47	2	D74393	hypothetical prote
35	36	11	2	27	2	D74393	hypothetical prote
36	36	11	2	27	2	D74393	hypothetical prote
37	36	11	2	27	2	D74393	hypothetical prote
38	36	11	2	27	2	D74393	hypothetical prote
39	36	11	2	27	2	D74393	hypothetical prote
40	36	11	2	27	2	D74393	hypothetical prote
41	36	11	2	27	2	D74393	hypothetical prote
42	36	11	2	27	2	D74393	hypothetical prote
43	36	11	2	27	2	D74393	hypothetical prote
44	36	11	2	27	2	D74393	hypothetical prote
45	36	11	2	27	2	D74393	hypothetical prote

## ALIGNMENTS

## RESULT 1

Lactase-phlorizin hydrolase 140K isoform \* rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Feb-1994 Sequence, revision 18-Nov-1994 Text, change 01-Nov-1996

R:Ratlet, M.A.; Hachey, D.L.; Quaroni, A.; Hutchins, T.W.; Nichols, B.L.; Rosenberger

J. Biol. Chem. 268, 13609-13616, 1993

A:Reference number: M46592; M46592; M46592; M46592; M46592

A:Accession: M46592

A:Status: preliminary

A:Residues: 1-19 (50%)

A:Note: sequence extracted from NCBI backbone (NCBI:P134560)

C:Keywords: carbohydrate digestion; intestinal

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

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Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;

Query Match: 14.4% Score 47; db 2; Length 19;







GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.  
OM protein - Protein search, using sw model  
Run on: January 28, 2003, 08:55:45 ; Search time 10 seconds  
251,006 Million coil updates/sec  
Title: us-09-730-465-2\_COPY\_20\_80  
Perfect score: 37.6UCPQISCFQIQVYWG.....DKVLELSEFSAFSPFNK 61  
Sequences:  
Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5  
Searched: 118892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 5368  
Minimum DB seq length: 0  
Maximum DB seq length: 61  
Post-processing: Minimum Match On  
Listing first 45 summaries  
Database : SwissProt\_40.4  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

No.	Score	Query	Match	Length	DB	ID	Description
1	44	13.5	22	1	CR31_LITSP	55628	litoria spi
2	41	12.5	35	1	PSBT_ORPSA	56238	litoria saliv
3	39	12.2	32	1	CR31_LITSP	55628	litoria spi
4	39	12.1	22	1	YABN_BACSI	56238	litoria spi
5	39	11.9	57	1	RR32_000SI	56238	litoria spi
6	38	11.8	57	1	PSBT_ORPSA	56238	litoria spi
7	38	11.8	57	1	PSBT_ORPSA	56238	litoria spi
8	37	11.3	22	1	CR31_LITSP	55628	litoria spi
9	37	11.3	31	1	PSBT_ORPSA	56238	litoria spi
10	37	11.3	31	1	PSBT_ORPSA	56238	litoria spi
11	37	11.3	49	1	Y502_BORBU	56238	litoria spi
12	37	11.3	49	1	Y502_BORBU	56238	litoria spi
13	37	11.3	49	1	Y502_BORBU	56238	litoria spi
14	37	11.3	49	1	Y502_BORBU	56238	litoria spi
15	36	11.0	31	1	SOUC_SFTRH	56238	litoria spi
16	36	11.0	31	1	SOUC_SFTRH	56238	litoria spi
17	36	11.0	31	1	THWV_NFNSA	56238	litoria spi
18	36	11.0	56	1	RL33_FICPR	56238	litoria spi
19	36	11.0	56	1	Y0Y_TTVI	56238	litoria spi
20	36	11.0	56	1	Y0Y_TTVI	56238	litoria spi
21	35	10.9	61	1	RL33_FICPR	56238	litoria spi
22	35	10.9	61	1	RL33_FICPR	56238	litoria spi
23	35	10.7	56	1	RL33_FICPR	56238	litoria spi
24	35	10.7	56	1	RL33_FICPR	56238	litoria spi
25	34	10.6	55	1	RL33_FICPR	56238	litoria spi
26	34	10.4	46	1	PRE_BACLI	56238	litoria spi
27	34	10.4	46	1	PRE_BACLI	56238	litoria spi
28	34	10.4	46	1	PRE_BACLI	56238	litoria spi
29	34	10.4	57	1	VIA_BVUS	56238	litoria spi
30	34	10.4	57	1	VIA_BVUS	56238	litoria spi
31	33	10.2	30	1	CAIM_LYFPA	56238	litoria spi
32	33	10.2	30	1	ATP8_LIMPO	56238	litoria spi
33	33	10.2	59	1	R17E_JHAKI	56238	litoria spi

US-09-730-465-2\_COPY\_20\_80  
Perfect score: 37.6UCPQISCFQIQVYWG.....DKVLELSEFSAFSPFNK 61  
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11	37	11.3	49	1	Y502_BORBU	56238	litoria spi
12	37	11.3	49	1	Y502_BORBU	56238	litoria spi
13	37	11.3	49	1	Y502_BORBU	56238	litoria spi
14	37	11.3	49	1	Y502_BORBU	56238	litoria spi
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16	36	11.0	31	1	SOUC_SFTRH	56238	litoria spi
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12	37	11.3	49	1	Y502_BORBU	56238	litoria spi
13	37	11.3	49	1	Y502_BORBU	56238	litoria spi
14	37	11.3	49	1	Y502_BORBU	56238	litoria spi
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29	34	10.4	57	1	VIA_BVUS	56238	litoria spi
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8	37	11.3	22	1	CR31_LITSP	55628	litoria spi
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10	37	11.3	31	1	PSBT_ORPSA	56238	litoria spi
11	37	11.3	49	1	Y502_BORBU	56238	litoria spi
12	37	11.3	49	1	Y502_BORBU	56238	litoria spi
13	37	11.3	49	1	Y502_BORBU	56238	litoria spi
14	37	11.3	49	1	Y502_BORBU	56238	litoria spi













15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 OS Striga hermonithica [Co:En] (CC 1.15.1.1) (fragments).  
 CC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Asteridae; Euasteridae; Lamiales; Orobanchaceae; Striga.  
 CC NCBI\_TaxID=68872;  
 RP SEQUENCE  
 KC TISSUE=Seedling;  
 RA Strasser, C., Corbett J.M., Dunn M.J., Totty M.F., Sterling A.,  
 RT "Identification of developmentally-specific markers in germinating and  
 RT haustorial stages of Striga hermonithica (Del.) Benth. seedlings.";  
 CC 1997, Plant Molecular Biology, 21: 111-119.  
 CC -1- FUNCTION: Destroys radicals which are normally produced within the  
 CC -1- cells and which are toxic to biological systems.  
 CC -1- CATABOLISM: Catabolism of organic compounds (C).  
 CC -1- COPHATOR: Copper and zinc (by similarity) - O(2) + H(2)O(2).  
 CC -1- SURCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- SUBCELLULAR STAGE: PREFERENTIALLY EXPRESSED IN GERMINATING  
 CC -1- SEEDLINGS.  
 DR InterPro: IPR001424; SOD\_CU\_ZN - PARTIAL.  
 DR PROSITE: PS00332; SOD\_CU\_ZN - PARTIAL.  
 KW Oxidoreductase; Copper; Zinc.  
 FT NON-CONS 17 18  
 FT NON-TER 31 31  
 SQ SEQUENCE 31 AA: 3109 MW: 407680889C2958 CMC54:  
 Query Watch 11.0%; Score 36; DB 1; Length 31;  
 Best Local Similarity 46.7%; Pred. No. 5.2e+02;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 Qy 18 VGVGVTFVFSNWPL 32  
 Db 31 VAGTITFANSQITL 25

Search completed: January 28, 2003, 08:59:43  
 Job Time : 12 secs





```

GN DBA.
OS Tapirus bairdii (baird's tapir).
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OX NBI_TaxID=5617.
RN NBI.
BA NBI.
FT "DNA polymorphism in the perissodactyla.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
FR From: PF00993; MNC_II_alpha.
FT NON_TER 60 60
FT SEQUENCE 60 AA: 6872 MW: 1548504813FAA91 CRC64:
Query Match 13.8% Score 45; DB 7; Length 60;
Best Local Similarity 30.0% Pred. No. 3.1e02;
Matches 12: Conservative 8; Mismatches 8; Indels 12; Gaps 2;
OY 20 GNTWHSVNLKVIKQKQKVALENSFRAFSK 59
DB 14 GDZIFHW-DNEKETYWLE-----EFOFASFE 41
RESULT 3
ID 098240 PRELIMINARY; PRT: 60 AA.
AC 098240: 1999 (TRENDEL, 10, Created)
DT 01-MAY-1999 (TRENDEL, 10, Last sequence update)
DT 01-DEC-2001 (TRENDEL, 19, Last annotation update)
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
GN DBA.
OS Tapirus indicus (Asiatic tapir) (Malaysian tapir).
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OX NBI_TaxID=9803.
RN NBI.
BA NBI.
FT "DNA polymorphism in the perissodactyla.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
FR From: PF00993; MNC_II_alpha.
FT NON_TER 60 60
FT SEQUENCE 60 AA: 6856 MW: 1545004813FAA91 CRC64:
Query Match 13.8% Score 45; DB 7; Length 60;
Best Local Similarity 30.0% Pred. No. 3.1e02;
Matches 12: Conservative 8; Mismatches 8; Indels 12; Gaps 2;
OY 20 GNTWHSVNLKVIKQKQKVALENSFRAFSK 59
DB 14 GDZIFHW-DNEKETYWLE-----EFOFASFE 41
RESULT 4
ID 098241 PRELIMINARY; PRT: 60 AA.
AC 098241: 1999 (TRENDEL, 10, Created)
DT 01-MAY-1999 (TRENDEL, 10, Last sequence update)
DT 01-DEC-2001 (TRENDEL, 19, Last annotation update)
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
GN DBA.
OS Buteo bicornis (black rhinoceros).
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OX NBI_TaxID=9803.
RN NBI.
BA NBI.
FT "DNA polymorphism in the perissodactyla.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

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RN SEQUENCE FROM N.A.
RA Fraser D.G., Ryder O.A.; Perissodactyla.
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OX EMBL: AF113549; A001968 1;
RN NBI.
BA NBI.
FT "DNA polymorphism in the perissodactyla.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
FR From: PF00993; MNC_II_alpha.
FT NON_TER 60 60
FT SEQUENCE 60 AA: 6870 MW: 15345005313FAA91 CRC64:
Query Match 13.8% Score 45; DB 7; Length 60;
Best Local Similarity 30.0% Pred. No. 3.1e02;
Matches 12: Conservative 8; Mismatches 8; Indels 12; Gaps 2;
OY 20 GNTWHSVNLKVIKQKQKVALENSFRAFSK 59
DB 14 GDZIFHW-DNEKETYWLE-----EFOFASFE 41
RESULT 5
ID 098242 PRELIMINARY; PRT: 60 AA.
AC 098242: 1999 (TRENDEL, 10, Created)
DT 01-MAY-1999 (TRENDEL, 10, Last sequence update)
DT 01-DEC-2001 (TRENDEL, 19, Last annotation update)
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
GN DBA.
OS Buteo bicornis (black rhinoceros).
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OX EMBL: AF113550; A001969 1;
RN NBI.
BA NBI.
FT "DNA polymorphism in the perissodactyla.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
FR From: PF00993; MNC_II_alpha.
FT NON_TER 60 60
FT SEQUENCE 60 AA: 6870 MW: 15345005313FAA91 CRC64:
Query Match 13.8% Score 45; DB 7; Length 60;
Best Local Similarity 30.0% Pred. No. 3.1e02;
Matches 12: Conservative 8; Mismatches 8; Indels 12; Gaps 2;
OY 20 GNTWHSVNLKVIKQKQKVALENSFRAFSK 59
DB 14 GDZIFHW-DNEKETYWLE-----EFOFASFE 41
RESULT 6
ID 098243 PRELIMINARY; PRT: 60 AA.
AC 098243: 1999 (TRENDEL, 10, Created)
DT 01-MAY-1999 (TRENDEL, 10, Last sequence update)
DT 01-DEC-2001 (TRENDEL, 19, Last annotation update)
DR InterPr: IP400103; MNC_II_alpha.
DR MNC class II DR-alpha (Fragment).
GN DBA.
OS Buteo bicornis (black rhinoceros).
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OC Buteo, Buteo, Chordata, Craniata, Vertebrata, Euteleostomi;
OX EMBL: AF113551; A001970 1;
RN NBI.
BA NBI.
FT "DNA polymorphism in the perissodactyla.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

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[illegible]



OS Streptococcus thermophilus bacteriophage DT1.  
OC Viruses: dsDNA viruses, no RNA stage; Caulovirales; Siphoviridae.

OC	OX	NCBI_TaxID=90410;
	RN	[[

RN [1]  
 CONFERENCE FROM N. S.

RP SEQUENCE FROM N.A.

RC STRAIN=DT1;

RX MEDLINE=99160757; PubMed=10049822; J.NEURAL-DE.

RX ABDO-CINE-991007377; PUBMED-10049822;  
 RA Tremblay D.-M.; Moineau S.;

HA Tremblay D.M., Moineau S.;  
ICOMLAB, Université Concordia, 1455

\*Complete genomic sequence of the RT

RT Streptococcus thermophilus

Virology 255:63-76

RN [2]

RN [Z] SEQUENCE FROM N A

RP  
SEQUENCE FROM N.A.

RC STRAIN=DT1;

RX MEDLINE=21382762; I

RA Duplessis M., Moineau S. :

\* Identification of a genetic deter

### Identification of a genetic determinant for chromosome 4p

RT specificity in *Streptococcus* therm

RL Mol. Microbiol. 41

RN [3]

RP SOURCE FROM N.A.

RP SEQUENCE FROM N.A.  
RC STRAIN=DT].

RC STRAIN=DTI;  
 GROUP=1 TO 4 M  
 MOD=1 TO 4 C

Qy 17 WYGNVTFHVP SNPLKEVLWKKQDKVAFLNSE 51

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045692 CT 1705PM

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AC Q45682;







XX 27-OCT-1999: 99US-0161734.  
 XX (CELS-) CEL-SCI CORP.  
 XX Zimmerman DH;  
 XX ZP 2001-374498/19.  
 XX Novel immunomodulatory peptide construct useful for modulating an  
 XX autoimmune disease, asthma or host-graft or graft-host disease  
 XX -  
 XX Claim 4: Page 28: 55pp: English.  
 XX The specification describes an immunomodulatory peptide construct  
 XX The immunomodulatory peptide comprises a first peptide associated with  
 XX autoimmune disease, allergy or asthma, or host-versus-graft rejection  
 XX which will bind to an antigen receptor on a set or subset of T cells,  
 XX and which will bind to an antigen receptor on a set or subset of T cells,  
 XX and which will bind to an antigen receptor on a set or subset of T cells,  
 XX immune response by the set or subset of T cells to which the first  
 XX peptide is attached. Alternatively, the second peptide will bind to a  
 XX set or subset of T cells to initiate, but not complete, an immune  
 XX response to cause the set or subset of T cells to undergo energy and  
 XX treatment of autoimmune disease, allergic reactions, asthma or  
 XX host-graft or graft-host rejection, or an immunomodulatory peptide  
 XX necessary to complete T cell activation. The present peptide is used to  
 XX construct immunomodulatory peptides of the invention, and is  
 XX representative of the second peptide.  
 XX Sequence 35 AA:  
 XX Query Match 27.5% Score 90; DB 22; Length 35;  
 XX Best Local Similarity 79.2%; Pred. No. 0.00023;  
 XX Matches 19; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 XX QY 35 VLKRGKQKVALEENSEPSSSF 58  
 XX 1 VLKRGKQKVALEENSEPSSSF 58  
 XX DB 1 VLKRGKQKVALEENSEGSSSY 24  
 XX  
 XX RESULT 4  
 XX ID ABB84077 standard; peptide: 17 AA.  
 XX AC ABB84077:  
 XX XX 06-AUG-2001 (first entry)  
 XX DE Immune modulating peptide causes a directed immune response.  
 XX XX Immunomodulatory peptide: immune response; autoimmune disease; allergy;  
 XX XX asthma; host-versus-graft rejection; T cell; anergy; apoptosis.  
 XX XX Unidentified.  
 XX XX W0200136448-A2.  
 XX XX 25-MAY-2001.  
 XX XX 27-OCT-2000; 2000MO-US41646.  
 XX XX 27-OCT-1999: 99US-0161734.  
 XX XX (CELS-) CEL-SCI CORP.  
 XX XX Zimmerman DH;  
 XX ZP 2001-374498/19.

XX WP1: 2001-374498/39.  
 XX Novel immunomodulatory peptide construct useful for modulating an  
 XX autoimmune disease, asthma or host-graft or graft-host disease  
 XX -  
 XX Claim 3: Page 37: 55pp: English.  
 XX The specification describes an immunomodulatory peptide construct  
 XX The immunomodulatory peptide comprises a first peptide associated with  
 XX autoimmune disease, allergy or asthma, or host-versus-graft rejection  
 XX which will bind to an antigen receptor on a set or subset of T cells,  
 XX and which will bind to an antigen receptor on a set or subset of T cells,  
 XX and which will bind to an antigen receptor on a set or subset of T cells,  
 XX immune response by the set or subset of T cells to which the first  
 XX peptide is attached. Alternatively, the second peptide will bind to a  
 XX set or subset of T cells to initiate, but not complete, an immune  
 XX response to cause the set or subset of T cells to undergo energy and  
 XX treatment of autoimmune disease, allergic reactions, asthma or  
 XX host-graft or graft-host rejection, or an immunomodulatory peptide  
 XX necessary to complete T cell activation. The present peptide is used to  
 XX construct immunomodulatory peptides of the invention, and is  
 XX representative of the second peptide.  
 XX Sequence 17 AA:  
 XX Query Match 26.6% Score 87; DB 22; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 0.00023;  
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 35 VLKRGKQKVALEENSE 51  
 XX 1 VLKRGKQKVALEENSE 17  
 XX DB 1 VLKRGKQKVALEENSE 17  
 XX  
 XX RESULT 5  
 XX ID ABB84085 standard; peptide: 32 AA.  
 XX AC ABB84085:  
 XX XX 06-AUG-2001 (first entry)  
 XX DE Immunomodulatory peptide used to treat Addison's disease.  
 XX XX Immunomodulatory peptide: immune response; autoimmune disease; allergy;  
 XX XX asthma; host-versus-graft rejection; T cell; anergy; apoptosis.  
 XX XX Addison's disease; steroid 21 hydroxylase.  
 XX XX Synthesis.  
 XX XX Key  
 XX XX Location/Qualifiers  
 XX XX Peptide 1-17  
 XX XX Peptide 18-22  
 XX XX Peptide 23  
 XX XX /note= "linker"  
 XX XX /note= "this residue represents amino acids 447-461  
 XX XX of the enzyme steroid 21 hydroxylase"  
 XX XX Peptide 24-31  
 XX XX /note= "linker"  
 XX XX /note= "this residue represents amino acids 477-491  
 XX XX of the enzyme steroid 21 hydroxylase"  
 XX XX W0300136448-A2.  
 XX XX 25-MAY-2001.  
 XX ZP 2001-374498/39.







[illegible]









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1 PRIOR APPLICATION NUMBER: PCT/US01/00668
2 PRIOR FILING DATE: 2001-01-30
3 PRIOR FILING DATE: 2001-01-30
4 PRIOR FILING DATE: 2001-01-30
5 PRIOR APPLICATION NUMBER: PCT/US01/00662
6 PRIOR FILING DATE: 2001-01-30
7 PRIOR FILING DATE: 2001-01-30
8 PRIOR APPLICATION NUMBER: PCT/US01/00663
9 PRIOR FILING DATE: 2001-01-30
10 PRIOR FILING DATE: 2001-01-30
11 PRIOR APPLICATION NUMBER: PCT/US01/00670
12 PRIOR FILING DATE: 2000-09-21
13 PRIOR FILING DATE: 2000-09-21
14 PRIOR APPLICATION NUMBER: US 60/234,697
15 PRIOR FILING DATE: 2000-06-30
16 PRIOR FILING DATE: 2000-06-30
17 PRIOR APPLICATION NUMBER: US 09/774,203
18 PRIOR FILING DATE: 2001-01-29
19 NUMBER OF SEQ ID NOS: 17
20 SOFTWARE: Anomax Sequence Listing Engine vers. I.1
21 SEQ ID NO 31465
22 TYPE: PRT
23 ORGANISM: Homo sapiens
24 OTHER INFORMATION: MAP TO AP00085.1
25 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
26 OTHER INFORMATION: EXPRESSED IN HELL00, SIGNAL = 1.8
27 OTHER INFORMATION: EXPRESSED IN HELL00, SIGNAL = 1.7
28 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
29 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
30 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
31 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
32 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
33 OTHER INFORMATION: EXPRESSED IN HELL00, SIGNAL = 1.7
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35 US-09-864-761-31465
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43 DB 2 ILWKKQKQDSLES 16
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45 RESULT 14
46 US-09-864-761-31626
47 Sequence 31626, Application US/09864761
48 Patent No. US2002048763A1
49 APPLICANT: Penn. Sharron G.
50 APPLICANT: Bank, David R.
51 APPLICANT: Bank, David R.
52 APPLICANT: Ch. No. 1
53 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
54 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
55 CURRENT APPLICATION NUMBER: US/09/864,761
56 CURRENT FILING DATE: 2001-05-23
57 PRIOR FILING DATE: 2000-02-04
58 PRIOR FILING DATE: 2000-02-04
59 PRIOR FILING DATE: 2000-02-04
60 PRIOR FILING DATE: 2000-02-04
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98 PRIOR FILING DATE: 2000-02-04
99 PRIOR FILING DATE: 2000-02-04
100 PRIOR FILING DATE: 2000-02-04

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1 PRIOR APPLICATION NUMBER: PCT/US01/00664
2 PRIOR FILING DATE: 2001-01-30
3 PRIOR FILING DATE: 2001-01-30
4 PRIOR FILING DATE: 2001-01-30
5 PRIOR APPLICATION NUMBER: PCT/US01/00665
6 PRIOR FILING DATE: 2001-01-30
7 PRIOR FILING DATE: 2001-01-30
8 PRIOR APPLICATION NUMBER: PCT/US01/00668
9 PRIOR FILING DATE: 2001-01-30
10 PRIOR FILING DATE: 2001-01-30
11 PRIOR APPLICATION NUMBER: PCT/US01/00662
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: PCT/US01/00661
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/00670
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR FILING DATE: 2000-09-21
19 PRIOR APPLICATION NUMBER: US 09/608,408
20 PRIOR FILING DATE: 2000-09-21
21 PRIOR APPLICATION NUMBER: US 09/774,203
22 PRIOR FILING DATE: 2001-01-29
23 NUMBER OF SEQ ID NOS: 4911
24 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
25 SEQ ID NO 31626
26 LENGTH: 35
27 ORGANISM: Homo sapiens
28 OTHER INFORMATION: MAP TO AP00923.1
29 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
30 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.2
31 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
32 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
33 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
34 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
35 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
36 OTHER INFORMATION: EXPRESSED IN HELL00, SIGNAL = 2.3
37 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
38 US-09-864-761-31626
39
40 Query Match 12.8% Score 42: DB 10: Length 35:
41 Best Local Similarity 46.7% Pred. No. 48:
42 Matches 7: Conservative 4: Mismatches 4: Indels 0: Gaps 0:
43
44 QY 35 VLWKKQKQVAVLEN 49
45 :||| ||| :|||:
46 DB 2 ILWKKQKQDSLES 16
47
48 RESULT 15
49 US-09-796-693-2346
50 Sequence 2346, Application US/09796692
51 Patent No. US20020198462A1
52 APPLICANT: Penn. Sharron G.
53 APPLICANT: Bank, David R.
54 APPLICANT: Bank, David R.
55 APPLICANT: Ch. No. 1
56 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
57 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
58 CURRENT APPLICATION NUMBER: US/09/796,692
59 CURRENT FILING DATE: 2001-05-23
60 PRIOR FILING DATE: 2000-02-04
61 PRIOR FILING DATE: 2000-02-04
62 PRIOR FILING DATE: 2000-02-04
63 PRIOR FILING DATE: 2000-02-04
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100 PRIOR FILING DATE: 2000-02-04

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OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 US-09-764-869-1235

Query Match 14.7% Score 48; DB 10; Length 57;  
 Best Local Similarity 30.6%; Pred. No. 15;  
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RESULT 4  
 US-09-799-514-19  
 : Sequence 19, Application US/0979514  
 : Patent No. US20020085220A1  
 : APPLICANT: Young et al.  
 : TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Amino Acid Sequences  
 : CURRENT APPLICATION NUMBER: US/09/799,514  
 : CURRENT FILING DATE: 2001-03-07  
 : PRIOR APPLICATION NUMBER: US-08-57/US00/21662  
 : PRIOR FILING DATE: 2000-08-27/US00/60152,248  
 : PRIOR APPLICATION NUMBER: 60/152,248  
 : PRIOR FILING DATE: 1999-09-03  
 : SOFTWARE: PatentL Ver. 2.0  
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 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : OTHER INFORMATION: MAP TO AC005817.1  
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 : OTHER INFORMATION: EXPRESSED IN HEART. SIGNAL = 6.4  
 : OTHER INFORMATION: EXPRESSED IN BRAIN. SIGNAL = 6  
 : OTHER INFORMATION: EXPRESSED IN BRAIN. SIGNAL = 6.5  
 : OTHER INFORMATION: EXPRESSED IN REIA. SIGNAL = 6.1  
 : OTHER INFORMATION: EXPRESSED IN PLACENTA. SIGNAL = 6.5, 5.9  
 : OTHER INFORMATION: EXPRESSED IN ADULT LIVER. SIGNAL = 6  
 : OTHER INFORMATION: EXPRESSED IN ADULT LIVER. SIGNAL = 6  
 : OTHER INFORMATION: SWISSPROT HIT: Q92183, EVALUATE 2.00e-20  
 : US-09-864-761-39695

Query Match 14.4% Score 47; DB 10; Length 51;  
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 DD 6 VLPLTQWLKALSLSSLNPRVPLAS 33

RESULT 5  
 US-09-864-761-39695  
 : Sequence 19955, Application US/09864761  
 : Patent No. US20020048763A1  
 : APPLICANT: Penn, Sharon G.  
 : APPLICANT: Bank, David K.  
 : APPLICANT: Bank, David K.  
 : APPLICANT: Chen, Wensheng  
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 : MICKONARRAY  
 : FILE REFERENCE: Aecolmca X-1  
 : CURRENT APPLICATION NUMBER: US/09/864,761  
 : PRIOR APPLICATION NUMBER: US 60/180,312  
 : PRIOR FILING DATE: 2000-02-04  
 : PRIOR APPLICATION NUMBER: US 60/207,456  
 : PRIOR FILING DATE: 2000-06-03  
 : PRIOR APPLICATION NUMBER: US 09/632,366  
 : PRIOR FILING DATE: 2000-06-03  
 : PRIOR FILING DATE: 2000-10-04  
 : PRIOR APPLICATION NUMBER: US 60/236,359  
 : PRIOR FILING DATE: 2000-10-04  
 : PRIOR APPLICATION NUMBER: PCT/US01/00666  
 : PRIOR FILING DATE: 2001-01-30  
 : PRIOR APPLICATION NUMBER: PCT/US01/00664  
 : PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21/09/608,408  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203  
 PRIOR FILING DATE: 2000-06-30  
 NUMBER OF SEQ ID NOS: 4311, 29  
 SOFTWARE: Annuance Sequence Listing Engine vers. 3.1  
 : SEQ ID NO 39695  
 : SEQ ID NO 39695  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : OTHER INFORMATION: MAP TO AC005817.1  
 : OTHER INFORMATION: EXPRESSED IN UING. SIGNAL = 6.4  
 : OTHER INFORMATION: EXPRESSED IN HEART. SIGNAL = 6.4  
 : OTHER INFORMATION: EXPRESSED IN BRAIN. SIGNAL = 6  
 : OTHER INFORMATION: EXPRESSED IN BRAIN. SIGNAL = 6.5  
 : OTHER INFORMATION: EXPRESSED IN REIA. SIGNAL = 6.1  
 : OTHER INFORMATION: EXPRESSED IN PLACENTA. SIGNAL = 6.5, 5.9  
 : OTHER INFORMATION: EXPRESSED IN ADULT LIVER. SIGNAL = 6  
 : OTHER INFORMATION: EXPRESSED IN ADULT LIVER. SIGNAL = 6  
 : OTHER INFORMATION: SWISSPROT HIT: Q92183, EVALUATE 2.00e-20  
 : US-09-864-761-39695

Query Match 14.1% Score 46; DB 10; Length 59;  
 Best Local Similarity 23.3%; Pred. No. 28;  
 Matches 8; Conservative 9; Mismatches 17; Indels 0; Gaps 0;  
 QY 10 FSOQITGVYGNVTFWNSVFAKVKKQK 43  
 |||||:||||:||||:||||:||||:||||:||||:||||:||||:  
 DD 8 FSDHYTQTSKKRLPIINDFIALEKRWRLUDE 41

RESULT 6  
 US-09-864-761-39725  
 : Sequence 19955, Application US/09864761  
 : Patent No. US20020048763A1  
 : APPLICANT: Penn, Sharon G.  
 : APPLICANT: Bank, David K.  
 : APPLICANT: Bank, David K.  
 : APPLICANT: Chen, Wensheng  
 : TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 : MICKONARRAY  
 : FILE REFERENCE: Aecolmca X-1  
 : CURRENT APPLICATION NUMBER: US/09/864,761  
 : PRIOR APPLICATION NUMBER: US 60/180,312  
 : PRIOR FILING DATE: 2001-02-23  
 : PRIOR APPLICATION NUMBER: US 60/207,456  
 : PRIOR FILING DATE: 2000-05-26  
 : PRIOR APPLICATION NUMBER: US 09/632,366  
 : PRIOR FILING DATE: 2000-06-03  
 : PRIOR APPLICATION NUMBER: US 60/236,359  
 : PRIOR FILING DATE: 2000-10-04  
 : PRIOR APPLICATION NUMBER: PCT/US01/00666  
 : PRIOR FILING DATE: 2000-09-21

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1 PRIOR FILING DATE: 2001-01-30
2 PRIOR APPLICATION NUMBER: PCT/US01/00667
3 PRIOR FILING DATE: 2001-01-30 / US01/00664
4 PRIOR FILING DATE: 2001-01-30 / US01/00664
5 PRIOR APPLICATION NUMBER: PCT/US01/00669
6 PRIOR APPLICATION NUMBER: PCT/US01/00665
7 PRIOR FILING DATE: 2001-01-30
8 PRIOR FILING DATE: 2001-01-30
9 PRIOR APPLICATION NUMBER: PCT/US01/00668
10 PRIOR APPLICATION NUMBER: PCT/US01/00663
11 PRIOR FILING DATE: 2001-01-30
12 PRIOR FILING DATE: 2001-01-30 / US01/00662
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: PCT/US01/00661
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: US 60/234,687
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: US 60/234,687
19 PRIOR FILING DATE: 2000-06-30
20 PRIOR APPLICATION NUMBER: US 09/608,408
21 PRIOR FILING DATE: 2001-01-29 / 09/774,203
22 PRIOR FILING DATE: 2001-01-29
23 NUMBER OF SEQ ID NOS: 49117
24 OTHER INFORMATION: Nucleic Acid Sequence Listing Engine vers. 1.1
25 SEQ ID NO 47,255
26 LENGTH: 33
27 TYPE: PRT
28 ORGANISM: Homo sapiens
29 FEATURE:
30 OTHER INFORMATION: MAP TO AC007115.1 SIGNAL = 18
31 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
32 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
33 OTHER INFORMATION: EXPRESSED IN BLOOD, SIGNAL = 1.1
34 OTHER INFORMATION: EXPRESSED IN BOLT ALGAL SIGNAL = 4
35 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
36 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
37 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.34
38 OTHER INFORMATION: SWISSPROT HIT: Q9X809, EVALU8 7.00e-05
39 OTHER INFORMATION: EST/JUMAN HIT: A755066.1, EVALU8 5.00e-05
40 US-09-864-761-34725
41 Query Match 13.3%, Score 43.5, DB 10: Length 33;
42 Best Local Similarity 26.3%, No. 29,
43 Matches 9; Conservative 10; Mismatches 12; Indels 3; Gaps 1;
44 Oy 27 USUWLEKLEVLKWKQWVALENSHAFSSNN 60
45 Db 1 PDLQPPDTLLDNNKNTETKDDFF---NLKM 31
46 RESULT 7
47 US-09-864-669-641
48 Patent No. US200206152A1
49 GENERAL INFORMATION:
50 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
51 FILE REFERENCE: EC007
52 CURRENT APPLICATION NUMBER: US/09/764,669
53 PRIOR FILING DATE: 2001-01-17
54 Prior application data removed - refer to PALM or file wrapper
55 NUMBER OF SEQ ID NOS: 2442
56 NUMBER OF SEQ ID LENGTH VER. 2.0
57 SEQ ID NO 641
58 LENGTH: 46
59 TYPE: PRT
60 ORGANISM: Homo sapiens
61 FEATURE:
62 NAME/KEY: SITE
63 LOCATION: (37)
64 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
65 US-09-764-669-641
66 Query Match 13.3%, Score 43.5, DB 10: Length 46;
67 Best Local Similarity 26.3%, No. 44;
68 Mismatches 10; Conservative 10; Indels 3; Gaps 1;
69 Oy 15 TGVVNYNTFF---HYFNVFLKLEVLK 37
70 Db 4 TGVVNNLLPVGISNVNNTYKLM 29
71 RESULT 8
72 US-09-864-761-33732
73 Sequence 33732, Appl Location US/0964761
74 Patent No. US2002061407A1
75 GENERAL INFORMATION:
76 TITLE OF INVENTION: GENOME-DERIVED OLIGOS, PEPTIDE ANALYSIS BY MICROARRAY
77 FILE REFERENCE: Aemila-4-1
78 CURRENT APPLICATION NUMBER: US/09/664,761
79 PRIOR FILING DATE: 2001-01-30
80 PRIOR APPLICATION NUMBER: US 60/180,312
81 PRIOR FILING DATE: 2000-02-04 / 60/207,456
82 PRIOR FILING DATE: 2000-05-26
83 PRIOR APPLICATION NUMBER: US 09/632,366
84 PRIOR FILING DATE: 2000-05-26
85 PRIOR APPLICATION NUMBER: GB 24363,6
86 PRIOR FILING DATE: 2000-10-04
87 PRIOR APPLICATION NUMBER: US 60/236,359
88 PRIOR FILING DATE: 2001-01-30
89 PRIOR APPLICATION NUMBER: PCT/US01/00666
90 PRIOR FILING DATE: 2001-01-30 / US01/00667
91 PRIOR FILING DATE: 2001-01-30
92 PRIOR APPLICATION NUMBER: PCT/US01/00664
93 PRIOR FILING DATE: 2001-01-30
94 PRIOR APPLICATION NUMBER: PCT/US01/00669
95 PRIOR FILING DATE: 2001-01-30
96 PRIOR APPLICATION NUMBER: PCT/US01/00665
97 PRIOR APPLICATION NUMBER: PCT/US01/00666
98 PRIOR FILING DATE: 2001-01-30
99 PRIOR FILING DATE: 2001-01-30 / US01/00663
100 PRIOR FILING DATE: 2001-01-30
101 PRIOR APPLICATION NUMBER: PCT/US01/00662
102 PRIOR FILING DATE: 2001-01-30
103 PRIOR APPLICATION NUMBER: PCT/US01/00661
104 PRIOR FILING DATE: 2001-01-30
105 PRIOR APPLICATION NUMBER: PCT/US01/00670
106 PRIOR FILING DATE: 2000-09-21
107 PRIOR APPLICATION NUMBER: US 60/234,687
108 PRIOR FILING DATE: 2000-06-30
109 PRIOR FILING DATE: 2000-06-30
110 PRIOR APPLICATION NUMBER: US 09/608,408
111 PRIOR FILING DATE: 2000-06-30
112 PRIOR APPLICATION NUMBER: US 09/774,203
113 NUMBER OF SEQ ID NOS: 49117
114 SOFTWARE: Autotax Sequence Listing Engine vers. 1.1
115 SEQ ID NO 33732
116 LENGTH: 47
117 TYPE: PRT
118 ORGANISM: Homo sapiens
119 FEATURE:
120 OTHER INFORMATION: MAP TO AL050337.6
121 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3

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*
* OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
* OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
* OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
* OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
* OTHER INFORMATION: EXPRESSED IN HELIO, SIGNAL = 1.6
* OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.84
* OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
* OTHER INFORMATION: EXPRESSED IN ADULT LUNG, SIGNAL = 1.0
* OTHER INFORMATION: SNAPSHOT HIT: 015260, EVALUATE: 0.00e-01
* OTHER INFORMATION: EST_HUMAN HIT: 00143746.1, EVALUATE: 9.00e-29
US-09-844-761-33732

Query Match
Best Local Similarity 13.3%; Score 43.5; DB 10; Length 57;
Matches 11; Conservative 1; Mismatches 8; Indels 7; Gaps 2;

Oy 19 YONTYFV---PNNVLEKAKDKVAVLENS 50
Dd 17 YCNISWDNDPEN-----SLWVAVAVQKQSSA 45

RESULT 9
US-09-815-242-10873
*
* Sequence 10873, Application US/09815242
* GENERAL INFORMATION
* APPLICANT: Haselbeck, Robert
* TITLE OF INVENTION: Prokaryotes
* CURRENT FILING DATE: 2001-03-21
* PRIOR FILING DATE: 2001-03-21
* PRIOR APPLICATION NUMBER: 60/131,078
* PRIOR FILING DATE: 2000-05-23
* PRIOR APPLICATION NUMBER: 60/207,727
* PRIOR FILING DATE: 2000-10-23
* PRIOR APPLICATION NUMBER: 60/242,578
* PRIOR FILING DATE: 2000-11-22
* PRIOR APPLICATION NUMBER: 60/227,931
* PRIOR FILING DATE: 2001-02-16
* NUMBER OF SEQ ID NOS: 14110
* SEQ ID NO 10873
* LENGTH: 34
* ORGANISM: Intercoccus faecalis

US-09-815-242-10873
Query Match
Best Local Similarity 13.0%; Score 43; DB 10; Length 34;
Matches 9; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 33 KEVIAKQKQKVALENSFAFSPKFR 61
Dd 3 ESIIIGAEKQKLELLWSWDFEDNARH 31

RESULT 10
US-10-001-835-147
*
* Sequence 147, Application US/10001835
* GENERAL INFORMATION
* APPLICANT: Salceda, Susana
* APPLICANT: Macina, Roberto
* APPLICANT: Cafferkey, Robert
* APPLICANT: Sun, Yongsheng
* TITLE OF INVENTION: Conditions and Methods Relating to Ovary Specific Genes and
* CURRENT APPLICATION NUMBER: US/10/001,835
* FILE REFERENCE: BEA-0777
* PRIOR FILING DATE: 2000-11-20
* PRIOR APPLICATION NUMBER: 60/249,597
* SOFTWARE: PatentL version 3.1
* SEQ ID NO 147
* LENGTH: 49
* ORGANISM: Homo sapien

US-10-001-835-147
Query Match
Best Local Similarity 13.0%; Score 42.5; DB 9; Length 49;
Matches 11; Conservative 9; Mismatches 13; Indels 7; Gaps 2;

Oy 10 FSQITGVVYGVNTHFWPSWFKVKAKQKVALENS 49
Dd 11 FQVQNTWISS---EYVQVHSUVCWTR-----SLLID 43

RESULT 11
US-09-844-761-42851
*
* Sequence 42851, Application US/0984761
* GENERAL INFORMATION
* APPLICANT: Penn, Sharon G.
* APPLICANT: Reik, David A.
* APPLICANT: Dard, David K.
* APPLICANT: Chen, Wensheng
* TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
* FILE REFERENCE: ANOVALC X.3
* CURRENT APPLICATION NUMBER: US/09/864,761
* PRIOR FILING DATE: 2000-02-04
* PRIOR APPLICATION NUMBER: US 60/180,312
* PRIOR FILING DATE: 2000-05-05
* PRIOR APPLICATION NUMBER: US 60/207,456
* PRIOR FILING DATE: 2000-08-03
* PRIOR APPLICATION NUMBER: US 09/632,366
* PRIOR FILING DATE: 2000-10-04
* PRIOR APPLICATION NUMBER: US 60/236,359
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00666
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00667
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00664
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00665
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00668
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00663
* PRIOR FILING DATE: 2001-01-30
* PRIOR APPLICATION NUMBER: PCT/US01/00662

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1 PRIOR APPLICATION NUMBER: PCT/US01/00661
2 PRIOR FILING DATE: 2001-01-30
3 PRIOR APPLICATION NUMBER: PCT/US01/00670
4 PRIOR FILING DATE: 2001-01-30
5 PRIOR APPLICATION NUMBER: US 60/234,687
6 PRIOR FILING DATE: 2000-09-21
7 PRIOR APPLICATION NUMBER: US 09/608,408
8 PRIOR FILING DATE: 2000-09-21
9 PRIOR APPLICATION NUMBER: US 09/774,203
10 PRIOR FILING DATE: 2001-01-29
11 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
12 SEQ ID NO 42851
13 LENGTH 59
14 TYPE: PR
15 ORGANISM: Homo sapiens
16 FEATURE:
17 OTHER INFORMATION: MAP TO AC006452.2
18 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
19 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
20 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
21 OTHER INFORMATION: EST_HUMAN HTI: BT78056.1, EVALU2 3.60e+00
22 US-09-864-761-12851

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Query Match 13.0%, Score 42.5; DB 10; Length 59;
Matches 11; Conservative 0; Mismatches 7; Indels 9; Gaps 1;
DB 11 CPQQO-----PPNNSSSSSKRY 28
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RESULT 12
US-09-864-761-13625
Sequence 33625, Application US/0984761
Patent No. US20020048753A1

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1 APPLICANT: Rank, David R.
2 APPLICANT: Penn, Sharron G.
3 APPLICANT: Chan, Weishang
4 APPLICANT: Chan, Weishang
5 FILE REFERENCE: ANOMAX-X
6 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
7 CURRENT APPLICATION NUMBER: US/09/864,761
8 PRIOR APPLICATION NUMBER: US 60/130,312
9 PRIOR FILING DATE: 2000-02-04
10 PRIOR APPLICATION NUMBER: US 60/207,456
11 PRIOR FILING DATE: 2000-08-03
12 PRIOR APPLICATION NUMBER: US 09/632,366
13 PRIOR FILING DATE: 2000-08-03
14 PRIOR APPLICATION NUMBER: US 60/236,359
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/00667
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/00664
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/00669
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/00663
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00662
25 PRIOR FILING DATE: 2001-01-30

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1 PRIOR APPLICATION NUMBER: PCT/US01/00661
2 PRIOR FILING DATE: 2001-01-30
3 PRIOR APPLICATION NUMBER: PCT/US01/00670
4 PRIOR FILING DATE: 2001-01-30
5 PRIOR APPLICATION NUMBER: US 60/234,687
6 PRIOR FILING DATE: 2000-09-21
7 PRIOR APPLICATION NUMBER: US 09/608,408
8 PRIOR FILING DATE: 2000-09-21
9 PRIOR APPLICATION NUMBER: US 09/774,203
10 PRIOR FILING DATE: 2001-01-29
11 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
12 SEQ ID NO 33625
13 LENGTH 34
14 TYPE: PR
15 ORGANISM: Homo sapiens
16 FEATURE:
17 OTHER INFORMATION: MAP TO AP00085.1
18 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
19 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
20 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
21 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
22 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
23 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
24 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.1
25 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
26 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
27 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
28 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
29 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
30 US-09-864-761-33625

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Query Match 12.8%, Score 43; DB 10; Length 34;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
DB 35 UUMKKKQGVAELEN 49
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RESULT 13
US-09-864-761-34155
Sequence 34155, Application US/09864761
Patent No. US20020048763A1

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1 APPLICANT: Rank, David R.
2 APPLICANT: Penn, Sharron G.
3 APPLICANT: Chan, David K.
4 APPLICANT: Chan, David K.
5 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TO
6 CURRENT APPLICATION NUMBER: US/09/864,761
7 PRIOR APPLICATION NUMBER: US 60/180,312
8 PRIOR FILING DATE: 2000-02-04
9 PRIOR APPLICATION NUMBER: US 60/207,456
10 PRIOR FILING DATE: 2000-08-03
11 PRIOR APPLICATION NUMBER: US 09/632,366
12 PRIOR FILING DATE: 2000-08-03
13 PRIOR APPLICATION NUMBER: US 60/236,359
14 PRIOR FILING DATE: 2000-09-27
15 PRIOR APPLICATION NUMBER: PCT/US01/00667
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00666
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00664
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00669
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00665
24 PRIOR FILING DATE: 2001-01-30

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1 APPLICANT: MURPHY, Randall B.  
 2 APPLICANT: Schuster, David I.  
 3 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
 4 INVENTOR: MURPHY, RANDALL B.; SCHUSTER, DAVID I.  
 5 NUMBER OF SEQUENCES: 348  
 6 CORRESPONDENCE ADDRESS:  
 7 ADDRESSEE: BROWDY AND NEWMARK  
 8 STREET: 1100 South Street, N.W., Suite 300  
 9 CITY: Washington  
 10 STATE: D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20004  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: Floppy disk  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 17 CONTACT PERSON: David I. Schuster  
 18 APPLICATION NUMBER: US/08/116,270  
 19 FILING DATE: 05-SEP-1993  
 20 PRIOR APPLICATION DATA: US 07/943,236  
 21 FILING DATE: 10-SEP-1992  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: BROWDY AND NEWMARK  
 24 REGISTRATION NUMBER: 34,033  
 25 REFERENCE/DOCKET NUMBER: MURPHY-2A  
 26 TELEPHONE: 202-428-9197  
 27 TELEFAX: 202-737-3528  
 28 INVENTOR: MURPHY, RANDALL B. ID NO: 307  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 45 amino acids  
 31 TYPE: amino acids  
 32 STRANDEDNESS: single  
 33 TOPOLOGY: linear  
 34 MOLECULE TYPE: peptide  
 35 US-08-116-270-307

Query Match 14/14; Score 46; Db 1; Length 45;  
 Local Similarity: 100%;  
 Matches: 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 14 YGVYGVGVHVP 27

Db 5 YGVGLGVLTPLP 18

Search completed: January 28, 2003, 09:01:40  
 Job time : 15 secs

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  OPERATING SYSTEM: IBM PC compatible
4  SOFTWARE: PatentIn Release #1.0, Version #1.25
5  CURRENT APPLICATION DATA: PC/US93/08528
6  APPLICATION NUMBER: US/08/118,270
7  FILING DATE: 09-SEP-1993
8  PUBLICATION NUMBER: US 07/943,236
9  PRIORITY DATE: 10-SEP-1992
10 ATTORNEY/AGENT INFORMATION:
11 REFERENCE/DOCKET NUMBER: MURPHY-2A
12 REGISTRATION NUMBER: 34,013
13 TELEPHONE: 202-628-5197
14 TELEFAX: 202-737-3528
15 INFORMATION FOR SEQ ID NO: 306:
16 LENGTH: 44 amino acids
17 STRANDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: Peptide
20 US-08-118-270-306
21
22 Query Match
23 Length: 44, Score 46; DB 1; Length 44;
24 Mismatches: 0; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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1 APPLICANT: WALLNER, Barbara P.
2 APPLICANT: MILLER, Glenn T.
3 APPLICANT: ROSA, Margaret D.
4 TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
5 NUMBER OF SEQUENCES: 43
6 CORRESPONDENCE ADDRESS:
7 STREET: 875 Third Avenue
8 CITY: New York
9 STATE: New York
10 COUNTRY: U.S.A.
11 ZIP: 10022-6250
12 COMPUTER READABLE FORM:
13 OPERATING SYSTEM: IBM PC compatible
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/460.132
16 PRIORITY INFORMATION:
17 CLASSIFICATION: 435
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/940.861
20 APPLICATION NUMBER: PCT/US92/02050
21 FILING DATE: 12-MAR-1992
22 FILING DATE: 07-OCT-1991
23 FILING DATE: 12-MAR-1991
24 FILING DATE: 07-OCT-1991
25 PRIORITY INFORMATION:
26 APPLICATION NUMBER: US 07/770.967
27 APPLICATION NUMBER: PCT/US92/02050
28 REFERENCE/DOCKET NUMBER: B151C1P2
29 TELEPHONE: (212)715-0673
30 TELEFAX: (212)715-0673
31 INFORMATION FOR SEQ ID NO: 2:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 50 amino acids
34 STRANDNESS: single
35 TOPOLOGY: linear
36 UNUSUAL: NO
37 ANTI-SENSE: NO
38
39 US-08-460-132-2
40
41 Query Match
42 Best Local Similarity 100.0%; Pred. No. 6,5e-27; Length 50;
43 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
44
45 Oy 10 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 59
46 Db 1 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 50
47
48 RESULT 6
49 PCT-US92-02050-2
50 5185441-1
51 PRELIM. NO. 5185441
52 APPLICANT: WALLNER, BARBARA P.; BESSONS, CATHERINE
53 INVENTOR: WALLNER, BARBARA P.; BESSONS, CATHERINE
54 MOLECULES AND PROCESSES FOR PRODUCING PL-LINKED LYMPHOCTE
55 FUNCTION ASSOCIATED ANTIGEN-3
56 CURRENT APPLICATION DATA:
57 APPLICATION NUMBER: US/07/237.309
58 FILING DATE: 26-AUG-1998
59 SEQ ID LENGTH: 38
60 5185441-1
61
62 Query Match
63 Best Local Similarity 100.0%; Pred. No. 2,9e-19; Length 38;
64 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
65
66 Oy 10 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 47
67 Db 1 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 38
68
69 RESULT 7
70 US-08-460-132-3

```

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1 STREET: 875 Third Avenue
2 CITY: New York
3 STATE: New York
4 COUNTRY: U.S.A.
5 ZIP: 10022-6250
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 OPERATING SYSTEM: IBM PC compatible
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: PCT/US92/02050
11 FILING DATE: 19920312
12 CLASSIFICATION: 435
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/667.971
15 FILING DATE: 12-MAR-1991
16 PRIORITY INFORMATION:
17 APPLICATION NUMBER: US 07/770.967
18 FILING DATE: 07-OCT-1991
19 PRIORITY INFORMATION:
20 ATTORNEY/AGENT INFORMATION:
21 REGISTRATION NUMBER: 27.794
22 REFERENCE/DOCKET NUMBER: B151C1P2
23 TELEPHONE: (212)715-0660
24 TELEFAX: (212)715-0673
25 INFORMATION FOR SEQ ID NO: 2:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 50 amino acids
28 STRANDNESS: single
29 TOPOLOGY: linear
30 UNUSUAL: NO
31 ANTI-SENSE: NO
32
33 PCT-US92-02050-2
34
35 Query Match
36 Best Local Similarity 100.0%; Pred. No. 6,5e-27; Length 50;
37 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
38
39 Oy 10 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 59
40 Db 1 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 50
41
42 RESULT 6
43 PCT-US92-02050-2
44 5185441-1
45 PRELIM. NO. 5185441
46 APPLICANT: WALLNER, BARBARA P.; BESSONS, CATHERINE
47 INVENTOR: WALLNER, BARBARA P.; BESSONS, CATHERINE
48 MOLECULES AND PROCESSES FOR PRODUCING PL-LINKED LYMPHOCTE
49 FUNCTION ASSOCIATED ANTIGEN-3
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER: US/07/237.309
52 FILING DATE: 26-AUG-1998
53 SEQ ID LENGTH: 38
54 5185441-1
55
56 Query Match
57 Best Local Similarity 100.0%; Pred. No. 2,9e-19; Length 38;
58 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
59
60 Oy 10 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 47
61 Db 1 FSDQIGVGVGVNTFVPSNPFLKVKKKQKVAELNSERAFSSFK 38
62
63 RESULT 7
64 US-08-460-132-3

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.  
OM protein - protein search, using sv model  
Run on: January 28, 2003, 08:58:45 ; Search time 14.5 seconds  
128-200 Million cell updates/sec  
Title: US-09-730-465-2\_COPY\_20\_80  
Perfect score: 337  
Sequence: 1 LKCFISFCFSQYGVVCG.....DKVAELSESPAFSSKFR 61  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 262574 seque, 2942292 residues

Total number of hits satisfying chosen parameters: 186412

Minimum DB seq length: 0  
Maximum DB seq length: 61

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Databases :  
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3: /cgn2\_6/prodate/1/isa/SA\_COMB.pep.\*  
4: /cgn2\_6/prodate/1/isa/SA\_COMB.pep.\*  
5: /cgn2\_6/prodate/1/isa/SA\_COMB.pep.\*  
6: /cgn2\_6/prodate/1/isa/SA\_COMB.pep.\*

Note: No. is the number of results predicted by chance to have a score greater than the observed score and is printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	260	79.5	50	1	US-07-440-861-2	Sequence 2, Appl 1
2	260	79.5	50	2	US-08-159-637-2	Sequence 2, Appl 1
3	260	79.5	50	2	US-08-159-637-2	Sequence 2, Appl 1
4	260	79.5	50	2	US-08-460-132-2	Sequence 2, Appl 1
5	260	79.5	50	5	PCT-US92-02050-2	Sequence 2, Appl 1
6	260	79.5	50	5	PCT-US92-02050-2	Sequence 2, Appl 1
7	62	19.0	29	1	US-08-328-152A-3	Sequence 3, Appl 1
8	54	16.5	11	6	51854412-270-36	Patent No. 5185441
9	54	16.5	11	6	51854412-270-36	Sequence 27, Appl 1
10	46	14.1	24	2	US-08-103-170-27	Sequence 27, Appl 1
11	46	14.1	44	1	US-08-118-270-305	Sequence 305, Appl 1
12	46	14.1	44	5	PCT-US93-08528-305	Sequence 305, Appl 1
13	46	14.1	44	5	PCT-US93-08528-305	Sequence 305, Appl 1
14	46	14.1	44	5	PCT-US93-08528-305	Sequence 305, Appl 1
15	46	14.1	45	1	US-08-118-270-307	Sequence 307, Appl 1
16	46	14.1	45	1	US-08-118-270-307	Sequence 307, Appl 1
17	46	14.1	47	1	US-08-118-270-308	Sequence 308, Appl 1
18	46	14.1	47	5	PCT-US93-08528-308	Sequence 308, Appl 1
19	46	14.1	47	5	PCT-US93-08528-308	Sequence 308, Appl 1
20	40.5	12.4	41	1	US-08-665-773-5	Sequence 5, Appl 1
21	40.5	12.4	41	4	US-08-400-716-2	Sequence 2, Appl 1
22	40.5	12.4	41	6	5177662-127-5	Sequence 5, Appl 1
23	40.5	12.4	41	6	5177662-127-5	Sequence 5, Appl 1
24	40	12.2	43	4	US-09-015-030-6	Sequence 6, Appl 1
25	39.5	12.1	41	1	US-07-709-031-1	Sequence 1, Appl 1
26	39.5	12.1	41	1	US-07-709-031-1	Sequence 1, Appl 1
27	39.5	12.1	41	1	US-07-709-031-5	Sequence 5, Appl 1

28 39.5 12.1 41 1 US-07-709-031-6  
Sequence 6, Appl 1  
29 39.5 12.1 41 1 US-07-709-031-6  
Sequence 6, Appl 1  
30 39.5 12.1 41 1 US-07-765-682A-4  
Sequence 4, Appl 1  
31 39.5 12.1 41 1 US-08-104-862-1  
Sequence 1, Appl 1  
32 39.5 12.1 41 1 US-08-104-862-1  
Sequence 1, Appl 1  
33 39.5 12.1 41 1 US-08-104-862-5  
Sequence 5, Appl 1  
34 39.5 12.1 41 1 US-08-104-862-6  
Sequence 6, Appl 1  
35 39.5 12.1 41 1 US-08-162-178-1  
Sequence 1, Appl 1  
36 39.5 12.1 41 1 US-08-260-846-22  
Sequence 22, Appl 1  
37 39.5 12.1 41 4 US-08-981-169B-9  
Sequence 9, Appl 1  
38 39.5 12.1 41 4 US-08-242-127-1  
Sequence 1, Appl 1  
39 39.5 12.1 41 4 US-08-242-127-1  
Sequence 1, Appl 1  
40 39.5 12.1 41 5 PCT-US92-05101-1  
Sequence 1, Appl 1  
41 39.5 12.1 41 5 PCT-US92-05101-1  
Sequence 1, Appl 1  
42 39.5 12.1 41 6 5177660-146-476-472  
Patent No. 5177660  
43 39.5 12.1 40 2 US-08-117-952-767  
Sequence 767, Appl 1  
44 39.5 12.1 58 3 US-08-076-124-48  
Sequence 48, Appl 1

## ALIGNMENTS

RESULT 1  
US-07-940-861-2  
Patent No. 5147853  
GENERAL INFORMATION:  
INVENTOR: MILLER, Glenn T.  
APPLICANT: MILLER, Glenn T.  
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE  
ANTIGEN 3  
NUMBER OF SEQUENCES: 43  
CLASSIFICATION: 514  
COUNTRY: U.S.A.  
STREET: 875 Third Avenue  
STATE: New York  
CITY: New York  
COMPUTER READABLE FORM  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: /07/940.861  
FILING DATE: 21-OCT-1992  
CLASSIFICATION: 514  
PRIORITY DATA: 514  
APPLICATION NUMBER: PCT/US92/02050  
FILING DATE: 12-MAR-1992  
PRIORITY DATA: US 07/667,971  
APPLICATION NUMBER: US 07/667,971  
FILING DATE: 12-MAR-1991  
PRIOR APPLICATION DATA: US 07/770,967  
FILING DATE: 07-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B15C1P2  
TELEPHONE CATALOG NUMBER: 15C1P2  
TELEPHONE: (212) 715-0608  
TELEFAX: (212) 715-0608  
INVENTOR: TO NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
STANDARDNESS: single



DR WPI: 1988-168634/51.  
 DR N-PS08: ANR1956.

XX DNA sequences encoding lymphocyte function associated antigen-3 -  
 XX which inhibits adhesion between T-lymphocytes and target cells.

XX Disclosures: 1: 46pp; English.

XX The polypeptide binds to CD2, the surface receptor of T-lymphocytes.  
 XX They also inhibit adhesion between T-lymphocytes and target cells.  
 XX They also interfere with the interaction of helper T-cells and antigen-presenting  
 XX cells and may be used to target specific T-cells for lysis and immune  
 XX target T-cells. Comparison of the sequence with the N-terminus of the  
 XX target T-cells suggests that amino acid 1-28  
 XX comprise a signal sequence and amino acid 29-222 is the mature LFA-3.  
 XX See also ANR1955 and 1956.

XX Sequence 250 AA:

Query Match 100.0%; Score 136; DB 9; Length 250;

Best Local Similarity 100.0%; Pred. No. 7-26-18; Mismatches 0; Gaps 0;

QY 1 MWAGSAGRALVSLVCLLHGFICFSQITGVYGVNTFVPSNPKLAKKKK 60  
 DB 1 MWAGSAGRALVSLVCLLHGFICFSQITGVYGVNTFVPSNPKLAKKKK 60

QY 61 DVALENSFAPSSFNKRYVLTZVSGSLITVLTSSDEDEYEMSPNITDMKFLV 120  
 DB 61 DVALENSFAPSSFNKRYVLTZVSGSLITVLTSSDEDEYEMSPNITDMKFLV 120

QY 121 LESLSPFTLCALNGLSVQCMTEPHNSHGLIWMSCPMCKCKNSTSTFMMND 180  
 DB 121 LESLSPFTLCALNGLSVQCMTEPHNSHGLIWMSCPMCKCKNSTSTFMMND 180

QY 181 LPQKLOCTLSNLPNTSSILLTCTPSSGSHRRVALPIPLAVITTCVLYNNGILAC 240  
 DB 181 LPQKLOCTLSNLPNTSSILLTCTPSSGSHRRVALPIPLAVITTCVLYNNGILAC 240

QY 241 DRKPFRTNSN 250  
 DB 241 DRKPFRTNSN 250

RESULT 2

ANR27161 standard; Protein, 250 AA.

ANR27161 standard; Protein, 250 AA.

ANR27161 standard; Protein, 250 AA.

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ANR27161 standard; Protein, 250 AA.

ANR27161 standard; Protein, 250 AA.

ANR27161 standard; Protein, 250 AA.

PN EP030648-A.  
 PD 16-SEP-1992.  
 PF 12-MAR-1992; 92EP-0104320.

PR 12-MAR-1992; 91US-0697971.  
 PS 07-OCT-1991; 91US-0770997.

PA (BIO) BIOGEN INC.

PI Miller GT, Rosa MD, Wallner BF;

PP US: 1992-089760/28.

PQ N-PS08: AQ28677.

PR CD2-binding domain of lymphocyte function associated antigen-3

PS auto-immune disease, e.g. systemic lupus erythematosus and

PT rheumatoid arthritis

PP Example 7: Fig 6; 85pp; English.

PS Transmembrane LFA-3 cDNA (previously sequenced) was used to

PP domain. One of the initial series of 30 nucleotide deletions

CC \*M57\* in which nucleotides 244-273 are deleted) gave rise to an

CC CD2-binding site removed. To investigate whether the region of

CC CD2-binding site removed. To investigate whether the region of

CC CD2-binding site removed. To investigate whether the region of

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CC CD2-binding site removed. To investigate whether the region of

CC CD2-binding site removed. To investigate whether the region of

XX Mature form: human; ovine; LFA-3; antiviral agent; virus; infection;  
 XX propagation cycle; HIV; PCR primer; sheep; homologue; DID; protein.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX 1..28 Peptide  
 XX Note= "Signal peptide"  
 XX Protein  
 XX Note= "Nature LFA-3"  
 XX JF06137331-A.  
 XX 03-JUN-1994.  
 XX 27-NOV-1992: 92JP-0318934.  
 XX 27-NOV-1992: 92JP-0318934.  
 XX (KAF) KANEHUCHI KAGAKU KOGYO KK.  
 XX WFI: 1994-021795-27.  
 XX NPSDB: AAQ03036.  
 XX An antiviral agent containing LFA-3 - useful on a virus with the  
 XX same infection propagation cycle as HIV.  
 XX Disclosure: Page 11-12: 18pp: Japanese.  
 XX This sequence represents the full length form of human LFA-3. This  
 XX protein contains a signal peptide and the D1, D2, TM and IC domains.  
 XX LFA-3 is an antiviral agent which is effective on a virus which has the  
 XX same infection propagation cycle as HIV. The antiviral activity of homologues of  
 XX this sequence was amplified by PCR. The homologues were pref. deletion mutants  
 XX of this sequence. The homologues have more distinct domains removed.  
 XX (See also AAQ03036-413 and AA060310-18).  
 XX Sequence 250 AA;  
 XX Query Match 100.0%; Score 1336; DB 15; Length 250;  
 XX Best Local Similarity 100.0%; Pred. No. 7.2e-18; Indels 0; Gaps 0;  
 XX Matches 250; Conservative 0; Mismatches 0;  
 OY 1 MWAGSDAGALGVSVCLLRGFCISCFQOITGVYGNVTFVSNVPLKIAKKOK 60  
 DB 1 MWAGSDAGALGVSVCLLRGFCISCFQOITGVYGNVTFVSNVPLKIAKKOK 60  
 OY 61 PNVAENAFASFNKRVVLYVQSCNIPYNSHGLINSMQCMQCKNKSITFMND 120  
 DB 61 PNVAENAFASFNKRVVLYVQSCNIPYNSHGLINSMQCMQCKNKSITFMND 120  
 OY 121 LLSLSPTLCALNGLSDVQCMIPYNSHGLINSMQCMQCKNKSITFMND 180  
 DB 121 LLSLSPTLCALNGLSDVQCMIPYNSHGLINSMQCMQCKNKSITFMND 180  
 OY 181 LPQKLOCTLNPLNTSSILITTCIPSSGSHRYALPIPLAVITTCIVYNGILAC 240  
 DB 181 LPQKLOCTLNPLNTSSILITTCIPSSGSHRYALPIPLAVITTCIVYNGILAC 240  
 OY 241 DRKDFPRTNS 250  
 DB 241 DRKDFPRTNS 250  
 ID RESUR 4  
 ID AA001370 standard; Protein: 250 AA.  
 XX AA001370;  
 XX 30-JUN-1997 (first entry)  
 DT

XX Human cell adhesion protein LFA-3.  
 XX human; T cell; MOLT-4; cell adhesion; LFA-3; immunosuppression;  
 XX cell line; immunosuppressant cell.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX 29..250 Peptide  
 XX /label= sig\_peptide  
 XX /label= nat\_peptide  
 XX M06633217-A1.  
 XX 24-OCT-1996.  
 XX 15-APR-1996: 96MO-JP01039.  
 XX 27-DEC-1995: 95JP-0341959.  
 XX 19-APR-1995: 95JP-0094060.  
 XX 04-JUL-1995: 95JP-0169110.  
 XX (KAF) KANEHUCHI KAGAKU KOGYO KK.  
 XX Fujiuchi T, Katsuchi T, Nishino T, Niwa H, Ohara T,  
 XX Okazaki T, Yamashita K,  
 XX WFI: 1996-048972-48.  
 XX NPSDB: AAQ39555.  
 XX Cell adhesion protein derived from LFA-3 - has immunosuppressant  
 XX activity and induces immunosuppressant cells when cultured in its  
 XX presence.  
 XX Example 2: Pages 63-64; 83pp: Japanese.  
 XX The present sequence is the human T cell line MOLT-4 (ATCC  
 XX CCR-1587) derived cell adhesion protein LFA-3, from which a claimed  
 XX 29 amino acid residue signal peptide has been removed. The signal  
 XX residues can be prepared. The protein has immunosuppressant  
 XX activity, and cells (e.g. T cells) cultured in its presence, and  
 XX immunosuppressant cells with potent immunosuppressant, but low side  
 XX effects.  
 XX Sequence 250 AA;  
 XX Query Match 100.0%; Score 1276; DB 17; Length 250;  
 XX Best Local Similarity 100.0%; Pred. No. 7.2e-18;  
 XX Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MWAGSDAGALGVSVCLLRGFCISCFQOITGVYGNVTFVSNVPLKIAKKOK 60  
 DB 1 MWAGSDAGALGVSVCLLRGFCISCFQOITGVYGNVTFVSNVPLKIAKKOK 60  
 OY 61 PNVAENAFASFNKRVVLYVQSCNIPYNSHGLINSMQCMQCKNKSITFMND 120  
 DB 61 PNVAENAFASFNKRVVLYVQSCNIPYNSHGLINSMQCMQCKNKSITFMND 120  
 OY 121 LLSLSPTLCALNGLSDVQCMIPYNSHGLINSMQCMQCKNKSITFMND 180  
 DB 121 LLSLSPTLCALNGLSDVQCMIPYNSHGLINSMQCMQCKNKSITFMND 180  
 OY 181 LPQKLOCTLNPLNTSSILITTCIPSSGSHRYALPIPLAVITTCIVYNGILAC 240  
 DB 181 LPQKLOCTLNPLNTSSILITTCIPSSGSHRYALPIPLAVITTCIVYNGILAC 240  
 OY 241 DRKDFPRTNS 250  
 DB 241 DRKDFPRTNS 250























[3] SEQUENCE OF 88-115 FROM N.A.  
TISUSP-fetal liver. PubMed:4361199;  
Takahashi N, Itoh S, Ohsa M, Nishida T, Nakai S, Hiroi T;  
"Structure of human immunoglobulin gamma genes: implications for  
evolution of a gene family.";  
[3] 25:671-675(1994).  
P P SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
L L EMBL 3: 1403-407(1982).  
P P MEDLINE-8421592; PubMed:6328676;  
MEDLINE-8421592; PubMed:6328676;  
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[illegible]

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 DR MM: 147130;  
 DR InterPro: IPRO03006; Ig\_MHC;  
 DR InterPro: IPRO03597; Ig\_c1;  
 DR Pfam: PF00447; Ig\_3-5L-like;  
 DR SMART: SM00410; IG-like; 1;  
 DR TrEMBL: A03116; AAA59374.1; AUF\_INT;  
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 Db 223 NVTQV 362  
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 Oy 283 NKLVSQV 323

## RESUME 6

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 DT 15-JUL-1996 (Rel. 38, Last annotation update)  
 OS Cavia porcellus (Guinea pig).  
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 RN [1]  
 RN [2] HUNCE OF 4-68  
 RX MEDLINE=71658471; PubMed=5538606;  
 RA Birbahein B.G., Inoué O.Z., Ceiba J.J.;  
 RT Immunoglobulin-G23. II. Amino acid sequence of the carboxyl-terminal  
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 RT Biochemistry 10:16-23(1971).  
 RN [3]  
 RN SEQUENCE OF 68-133 AND 312-339.  
 RX MEDLINE=71058488; PubMed=5538616;  
 RA Birbahein B.G., Inoué O.Z., Ceiba J.J.;  
 RT "Structure of heavy chain from strain 13 guinea pig  
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 CC 11. BRED GUINEA PIGS.

DR PIR: A02151; Q20P  
 DR HESP; R01842; 7FA8  
 DR InterPro: IPR001806; IG\_MHC.  
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 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00407; Ig\_2.  
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 DR PROSITE: PS00290; IG\_MHC; 1.  
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 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
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 Db 44 SGLTSSQVTFVAVQLSGLTSSVNTVSSOKATCAVH-----ASSTK-----VKTVPET 97  
 Oy 124 -----HCPAPVQLGSGVTLFFPKFKDTISRTPEVTCVVDVSHSDVSEKFNVDVCHN 176  
 Db 98 RFLPEPCTCPCHPBNLGGQVFFPKFKDLATSEDTCTVVDVSDQSPVQVFTNNEQVPT 157  
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 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 38, Last annotation update)  
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 OS Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX NCBI\_TaxId=10090.  
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